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A; Accession: JC5917
                                                                                                                                                                                                                                                                                                                                                                                                                                  셤
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hepatic lectin homolog (BamHI-ORPB) - fowlpox virus (isolate HP-438[Munich])
C;Species: fowlpox virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C;Accession: H12963
R;Tomley, F; Binns, M; Campbell, J; Boursnell, M.
J;Gen. Virol. 69, 1025-1040, 1988
A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpox A;Reference number: JT0442; MUID:88229622; PMID:2836548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A.Molecule type: protein
A;Residues: 1-125 <MAT>
A;Residues: 1-125 <MAT>
A;Residues: 1-125 <MAT>
A;Residues: 1-126 <MAT>
B;Residues: 1-126 <MAT>
B;Residues: 1-127 <MAT>
B;Ratsui, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fujimura, Y.; Oz
Res. Commun. Biochem. Cell Mol. Biol. 1, 271-284, 1997
A;Title: Complete amino acid sequence of bitiscetin, a novel von Willebrand factor modul
A;Reference number: JC5916
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Y.; 0z
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                                                   60-Val, 61-Lys, 80-Glu, 131-His,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        K.; Fujimura,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               willebrand
                                                                                                                                                                                                                                                           8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ξ,
                                                                                                                                                                                                                                                                                                           75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTF---PDNQGVKLFGEYLGQDF- 130
                                                                                                                                                                                                                                                                                                                                                                                                                           131 YWIGLR--NIDG-WRWEGGPALSLRILTN------SLIQRCGAIHR-----NGLQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 YWLGASDINIEGRWLWEGQRRMX---YTNWSPGQPDNAGGIEHCLELRRDLGNYLWNDYQ 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PSCPILWTRNG----SHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLG 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | : : | | | | : : : : | | | | : DIKILYCKEGWVGYNKNCYFFSEEKNNKSLAVERCKDMDGHLTSISSKEEFKFILRYKG 100
                                                                                                                                                                                                                                                                                                                                                Ditiscetin beta chain - puff adder
Ditiscetin beta chain - puff adder
Ditiscetin beta arietans (puff adder)
C;Species: Bitis arrietans (puff adder)
C;Species: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 12-Feb-1999
C;Accession: JC5059; JC5917
R;Matsul, T.; Hamako, J.; Suzuki, M.; Hayashi, N.; Ito, M.; Makita, K.; Fuji A;Description: Complete amino acid sequence of bitiscetin, a novel von wille A;Reference number: JC5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:D00295; NID:g221380; PIDN:BAA00203.1; PID:g221394
C;Superfamily: fowlpox virus hepatic lectin homolog; C-type lectin homology
C;Keywords: early protein
F;48-116/Domain: C-type lectin homology #status atypical <LEC>
                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5;
                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          th 10.4%; Score 107.5; DB 1; Length 116; Similarity 29.2%; Pred. No. 0.0024; 21; Conservative 14; Mismatches 32; Indels 5;
                                                                                                                                                                                                 Length 155;
                                                                                                                                                                                                                                                        Indels
               A, Residues: 1-155 cMAN>
A, Rocie 4-Pro, 4-Ile, 9-His, 11-Gly, 20-Arg, 45-Asp, 60-Val, 65. Superfamily: tetranectin; C-type lectin homology
F,1-155/Product: perlucin #status experimental cMAL>
F,1-155/Region: 10-residue repeats (N/D-S-L-H-A-N-L-Q-R)
                                                                                                                                                                                        Query Match 10.6%; Score 109.5; DB 2; Best Local Similarity 26.9%; Pred. No. 0.0021; Matches 36; Conservative 21; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               172 ASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---COKPSHFICEK 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          128 QDFYWIGLRNID 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 PGNHWİĞIEKVD 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Accession: H29963
A;Molecule type: DNA
A;Residues: 1-116 <TOM>
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Best Local :
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Matches
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129 DFYWIGLRNIDGW-----RWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVA---- 178
                                                                                                                                                                                                                                                                                                                                                                                                                                      ---CFVAESFHN 106
                                                                                                                                                                                                                                                                                                                                          63
                                                                     C;Comment: This protein is a modulator of a von Willebrand factor modulator. C;Superfamily: tetranectin, C-type lectin homology C;Reywords: venom F;4-121/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                        79 WIRNGSHCYYFSMEKKDWNSSLKFCAD--KGSHLLIFPDNQGVKLFGEYLGQ--
                                                                                                                                                                                            Length 125;
                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                               DB 2;
                                                                                                                                                                                            10.3%; Score 105.5; DB 2; 24.8%; Pred. No. 0.0042; tive 15; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                   64 VLVWIGLSHF--WRICPLRWTDGARLDYRALSDEPI--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: August 10, 2004, 16:44:40
Job time : 14.5 secs
                                                                                                                                                                                                                                              Conservative
A,Molecule type: protein
A,Residues: 1-125 <MA2>
A,Experimental source: venom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  --LQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 KWIQWTCNR 115
                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 32; Conserv
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7;

(010/811) AUDIO 0600 5/4/

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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sw model - protein search, using protein ĕ

(without alignments) 1223.649 Million cell updates/sec August 10, 2004, 16:36:04; Search time 8 Seconds Run on:

US-09-811-367B-3 Title: Perfect score:

1 MADSSIYSTLELPEAPQVQD......GLQASSCEVALQWICKKVLY 188 Sequence:

BLOSUM62

Scoring table:

141681 seqs, 52070155 residues Gapop 10.0 , Gapext 0.5 Searched: Total number of hits satisfying chosen parameters:

length: Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries length: 188

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Quarkey macaca mula Q13241 homo sapien Q9m241 pan troglod P23807 trimeresuru 093427 crotalus du P14371 fowlpox vir Q94137 dewlpox vir Q94137 dewlpox vir Q94189 aqkistrodon P14370 fowlpox vir P81397 agkistrodon P81398 agkistrodon P81399 megabalanus P09439 megabalanus P09439 megabalanus P81596 cottalus norv P81508 crotalus norv P81563 crotalus norv P81563 crotalus norv P25031 rattus norv
SUMMARIES	CD94 MACMU CD94 HACMU CD94 ENUTR IXB TRIFL CVXE CRODU VX39 FOWPV WHE AGKHA CLEZ HUMAN WHEA AGKHA VOOB FOWPV RHCA AGKRH CRODE CRODE COTHE CRODE COTHE CRODE COTHE CRODE RHCE AGKRH ABA3 TRIAB BOTTA BOTTA BOTTA BOTTA RHCE AGKRH ABA3 TRIAB EVXA TRIFL BOTTA BOTTA RHCE AGKRH ABA3 TRIAB EVXA TRIFL EALLA ABA3 TRIPL EALLA ABA3 TRIPL IXA TRIFL IXA TRIFL IXA TRIFL IXA TRIPL IXA TRIPL CHAB COUNCE FARI CHAB COUNCE CROAT CHAB CROAT CHAB CROAT CROAT CHAB CROAT C
DB	;
Length	179 179 179 179 179 179 179 183 183 185 185 185 185 185 185 185 185 185 185
% Query Match	7. 7. 7. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4. 4.
Score	180 - 1
Result No.	: : : : : : : : : : : : : : : : : : :

EMBL; AF190931; AAF74527.1; -. EMBL; AF190932; AAF74528.1; -.

P81116 trimeresuru	Q95mil pan troglod	P05140 hemitripter	043908 homo sapien	Q92778 mesocricetu	P05451 homo sapien	P48304 homo sapien	P81017 echis carin	Q9psn0 bitis ariet	Q9psm4 lachesis st	P23132 bos taurus	P81115 trimeresuru
ABBB TRIAB	NKGF PANTR	ANP HEMAM	NKGF HUMAN	PBCG_MESAU	LITA_HUMAN	LITB_HUMAN	ECHA_ECHCA	LECG_BITAR	LECG_LACST	LITH_BOVIN	ABBA_TRIAB
Н	Н	٦	Н	Н	Н	Н	Н	1	۲	7	1
118	158	163	158	175	166	166	133	135	135	175	132
9.1	0.6	0.6	8.9	8.8	8.7	8.7	8.4	8.4	8.4	8.4	8.3
93.5	93	93	92	91	90	89.5	86.5	98	86	86	85.5
34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=21158386; PubMed=11261935; Kravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.; Sravitz R.H., Grendell R.L., Slukvin I.I., Golos T.G.; Spiression of NKG2-A and NKG2-C mRNAs and novel alternative splicing of 5' exons in rhesus monkey decidua."; Immunogenetics 53:69-73(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ບັ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells. -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
                                                                                                 Q9MZK9; Q9GK91; Q9MZK7; Q9MZK8; 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update) Natural killer cells antigen CD94 (NK cell receptor) (Killer cell lectin-like receptor subfamily D, member 1).
                                                                                                                                                                                                                                                                                                                                                                                     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae;
Cercopithecinae; Macaca.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           [1]

SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).

MEDLINE=20322487; PubMed=10866118;

LaBonte M.L., Levy D.B., Letvin N.L.;

"Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B, and D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pertablicative splicing; Named isoforms=3; Name=1; Synonyms=CD94-A; Isold=Q9MXS9-1; Squence=Displayed; Name=2; Synonyms=CD94-B; Isold=Q9MXK9-2; Sequence=VSP_003055; Name=3; Synonyms=CD94 alt; Isold=Q9MXS9-3; Sequence=VSP_03054; Isold=Q9MXS9-3; Sequence=VSP_030554; Isold=Q9MXS9-3; Isold
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           members.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                   179 AA.
                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Immunogenetics 51:496-499(2000).
                                                                                                                                                                                                                                                                                                                                                       Macaca mulatta (Rhesus macaque)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   [2]
SEQUENCE FROM N.A. (ISOFORM 1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                             KLRD1 OR CD94.
                                                                   MACMU
RESULT 1
CD94 MACMU
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AJ000001; CAA03845.1; -. AB009597; BAA24450.1; -. AB010084; BAA24451.1; -. BC028009; AAH28009.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PDB; 1B6E; 15-JUN-99.
                                                      Biassoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL;
EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL;
  85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                                                                                                                                                                                                                                                71 NCYFISSEEKTWNESRHFCASOKSSLLOLONRDELDFMSS--SQHFYWIGLSYSEEHTAW 128
                                                                                                                                                                                                                                                                                                                                                        70
                             InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT_T 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS00611; C_TYPE_LECTIN_2; 1.
Autigen; Receptor; Glycoprotein_Transmembrane; Signal-anchor; Lectin; Alternative splicing; Polymorphism.
                                                                                                                                                                                                N-LINKED (GLCNAC. . .) (POTENTIAL).
MAVFKTTLWRLISGTLGIICLSLMATLGILLKNS -> MAA
                                                                                                                                                                                                                                                                                                                                     ----KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                        14 GTLGIICLSLMATLGILLKNSFTKLSVEPAYTPGPNIELQKDSDC--C-SCHEKWVGYRC
                                                                                                     CYTOPLASMIC (POTENTIAL).
SIGNAL-ANCHOR (TYPE-11 MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Blood;
MEDLINE=96011848; PubMed=7589107;
Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CD94_HUMAN STANDARD, PRT; 179 AA.

013241, 043321, 04373; 09UBE3; 09UBQ0;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
NAUVALOGO (Rel. 43, Last annotation update)
Natural killer cells antigen CD94 (NK cell receptor Subfamily D, member 1) (KP94).
                                                                                                                                  EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIV (LONG PORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                               31;
                                                                                                                                                                                                                                                                                                                                                                                                                       142 RWEGGPALSLRILTNSLI---QRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                  129 IMENGSALSQYLFPSFETFKPKNCIAYNSKGNALDESCETKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Placenta;
MEDLINE=98139529; PubMed=9472066;
Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular characterization of human CD94: a type II membrane glycoprotein related to the C-type lectin superfamily."; Eur. J. Immunol. 25:2433-2437(1995).
                                                                                                                                                                                                                                                                                            ; Score 180.5; DB 1; Length 179;
; Pred. No. 6e-11;
17; Mismatches 68; Indels 31
                                                                                                                                                                                                                                                                        06212B4494527F07 CRC64;
                                                                                                                                                                                                                                         (in isoform 2).
                                                                                                                                                                                                                                                  FTIG=VSP_003055.
                                                                                                                                                                                                                               FTIG=VSP 003054.
                                                                                                                                                                                                                      (in isoform 3
                                                                                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                    44 GLLTVILMSLLMYQRILCCGS------
                                                                                                                                                                                                                                           으
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                        20607 MW;
                                                                                                                                                                                                                                                                                           ch 17.5%;
1 Similarity 31.8%;
54; Conservative 1
EMBL; AF190933; AAF74529.1;
EMBL; AF294886; AAG34498.1;
HSSP; P22897; 1EGG.
                                                                                                    31
                                                                                                                                                                                                                                           105
                                                                                                                                   179
176
72
174
166
83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Human)
                                                                                                                                                                                                                                                                       179 AA;
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                          105
                                                                                                                                   32
98
61
89
152
132
                                                                                                                                                                                                                                                             139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KLRD1 OR CD94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lanier L.L.;
                                                                                                     DOMAIN
TRANSMEM
                                                                                                                                                       DISULFID
                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                CARBOHYD
                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                              VARIANT
                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD94 HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RICHARDLINE=22388257; PubMed=12477932;
RICHARDLINE=22388257; PubMed=12477932;
RICHARDLINE=22388257; PubMed=12477932;
RA Altschul S.F., Zeeberg B., Batcow K.H., Schaefer C.R., Bhat N.K.,
RA Altschul S.F., Zeeberg B., Batcow K.H., Schaefer C.F., Bhat N.K.,
RA Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Haich F.,
RA Bottchench M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Stapleton M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.B., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Chards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Chards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.M.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Marra M.A.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA Cheneration and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99267245; PubMed=9601951; Purukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., Tadokoro K., Tohma S., Inoue T., Yamamoto K., Juji T.; "A alternatively spliced form of the human CD94 gene."; Immunogenetics 48:87-88(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
-!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
-!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          --- SUBCELLULAR LOCATION: Type II membrane protein.
--- ALTERNATIVE PRODUCTS:

Event-Alternative spliding; Named isoforms=3;

Rame=1; Synonyms=CD94-A;

Isold=Q13241-1; Sequence=Displayed;

Name=2; Synonyms=CD94 -B;

Isold=Q13241-2; Sequence=VSP_003053;

Name=3; Synonyms=CD94 alt;

Isold=Q13241-3; Sequence=VSP_003052;

--- TISSUB SPECIFICITY: Natural killer cells.
--- TISSUB SPECIFICITY: Natural killer cells.
--- SIMILARITY: Contains 1 C-type lectin family domain.
--- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;

WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd94.htm".
                                                                                                                                                                                                                                                                                 Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
Lehrach H., Francis F., Lopez-Botet M.; "Structure of the human CD94 C-Type lectin gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
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Y14288; CAA74663.1; JOINED.
                                                                                            Immunogenetics 47:305-309(1998).
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                                                                                                                                                                                              (ISOFORM 2)
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                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 3)
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                                                                                                                                                                                         SEQUENCE FROM N.A.
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            MINI, 602894; -.

R GO; GO:0005866; C:plasma membrane; TAS.

GO; GO:0005866; P:antimicrobial humoral response (sensu Inver...; TAS.)

BR GO; GO:0005960; P:antimicrobial humoral response (sensu Inver...; TAS.)

BR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.)

BR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.)

BR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.)

BR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.)

BR GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.)

BR ROSITE; PS00615; C TYPE LECTIN 1; FALSE NGG.

BR ROSITE; PS00615; C TYPE LECTIN 2; 1.

BR Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin; KW Alternative splicing; 3D-structure.

RW Alternative Splicing; 3D-structure.

RW Alternative Splicing; SIGNAL-ANCHOR (TYPE-II MEWBRANE PROTEIN)

FT TRANSMEM 11 31 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71 NCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEEHTAW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HCYYFSMEKKDWNSSLKFCADKGSHLLTFFDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-LINKED (GLCNAC. .) (POTENTIAL).
MAVFKTTLWRLISGTLGIICLSLMATLGILLKNS -> MAA
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28-FEB-2003 (Rel. 41, Last sequence update)
29-OCT-2003 (Rel. 42, Last annotation update)
Natural killer cells antigen CD94 (NK cell receptor) (Killer cell
lectin-like receptor subfamily D, member 1).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLUNG. . . ) (POTENTIAL).
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Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
Parham P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 RWEGGPALSLRILIN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Rapid evolution of NK cell receptor systems demonstrated by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. 9.5e-11;
; Mismatches 68; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  L -> LQ (In isoform 2).
/FTId=VSP_003053.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17.3%; Score 178.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44 GLLTVILMSLLMYQRILCCGS-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             comparison of chimpanzees and humans.";
Immunity 12:687-698(2000).
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MEDLINE=21623889; PubMed=11751968;
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Genew; HGNC:6378; KLRD1
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VARSPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; APZ59054; AAR86964.1; -.

HSSP; P22897; IEGG
InterPro; IPR001304; Lectin_C.

Pfan; PF00059; lectin_c; 1.-

SMART; SM00034; CLCTT; 1.-

PROSITE; PS00615; CTYPE LECTIN 1; FALSE_NEG.

PROSITE; PS50041; CTYPE LECTIN 2; 1.-

Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin; Alternative splicing 1.0 CYTOPLASMIC (POTENTIAI.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 GLLTVILMSLLMYQRILCCGS------KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTLGIICLSLMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCQEKWVGYRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYTOPLASMIC (POTENTIAL)
SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
(POTENTIAL)
                                                                                                                                                -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.
Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guethlein L.A., Uhrberg M., Parham P.; "Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
L -> LQ (in isoform 2).
/FTId=VSP_003056.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17.3%; Score 178.5; DB 1; Length 179; 31.8%; Pred. No. 9.5e-11; ive 17; Mismatches 68; Indels 31.
                                                                                                                                                                                                                                                                                                                                                                                                                Isoid=Q9MZ41-1; Sequence=Displayed;
Name=2; Synonyms=CD94-B;
Isoid=Q9MZ41-2; Sequence=VSP 003056;
TISSUE SPECIFITY: Sequence=VSP siller cells.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7244D99E8D9587E7 CRC64;
                                                                                                                                                                                                                                                                  -!- SUBCELLULAR LOCATION: Type II membrane protein.
                                                                                                                                                                                                                                                                                                                    Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ä.
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P23807; Q91247;
01-NOV-1991 (Rel. 20, Created)
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                                                                                                                        J. Immunol. 168:240-252 (2002)
                                                                                                                                                                                                                                                                                                                                                                                           Name=1; Synonyms=CD94-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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NCBI_TaxID=8732;
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                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97331317; PubMed=9187649; Mizuno H., Atoda H., Morita T.; Mizuno H., Pulimoto Z., Koizumi M., Kano H., Atoda H., Morita T.; Mizuno H., Pulimoto Z., Koizumi M., Kano H., Atoda H., Morita T.; of C-type lectin domains."; Nat. Struct. Biol. 4:438-441(1997).

-I Struct. Biol. 4:438-441(1997).

-I FUNCTION: Anticoagulant protein which binds with factor IX and factor X in the presence of calcium with a 1 to 1 stoichiometry.

-I SUBCELULIAR LOCATION: Secreted.

-I SUBCELLULAR LOCATION: Secreted.

-I MISCELLANBOUS: Calcium is required for ligand binding.
                                                                                                              | IJ

SEQUENCE FROW N.A.

MEDLINE=96184662; PubMed=8645314;

Matsuzaki R., Yoshihara B., Yamada M., Shima K., Atoda H., Morita T.;

"CDNA, cloning of IX/X-BP, a heterogeneous two-chain anticoagulant

"CDNA, cloning of IX/X-BP, a heterogeneous two-chain anticoagulant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COAGULATION FACTOR IX/FACTOR X-BINDING
                                                           Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Epidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea; Viperidae, Crotalinae, Trimeresurus.
                                                                                                                                                                                                                           MEDLINE=91332000; PubMed=1831197;
Atoda H., Hyuga M., Morita T.;
"The primary structure of coagulation factor IX/factor X-binding
protein isolated from the venom of Trimeresurus flavoviridis.
Homology with asialoglycoprotein receptors, proteoglycan core
protein, terranectin, and lymphocyte Fc epsilon receptor for
immunoglobulin E.";
15-JUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Coagulation factor IX/factor X-binding protein B chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-TYPE LECTIN (LONG FORM).

BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

INTERCHAIN (WITH C-102 IN A CHAIN).

BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROTEIN B CHAIN
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PDB; 1IXX, 06-MX-98.
PDB; 1IXX, 06-MX-98.
INCEPPO; 1BM001304; Lectin_C.
INCEPPO; 1PR001304; Lectin_C.
INCEPPO; 1PR001399; PANCHEATIS_AC.
PRINTS; PR01504; PRCREATISAP.
SWART; SW00034; CLECT; 1.
PR0SITE; PS00615; C_TVPE_LECTIN 1; 1.
PROSITE; PS00615; C_TVPE_LECTIN 1; 1.
Lectin; Calcium; Signal; 3D-structure.
                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                 Biol. Chem. 266:14903-14911(1991).
                                               Trimeresurus flavoviridis (Habu)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D83332; BAA11888.1; -.
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1988
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 DWNSSLKFCADK--GSHLLTFPDNQG----VKLFGEYLGQDFYWIGLRNI---DGWRWEG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -----SLSGTAADCPSD---WSSYEGHCYKPFSEPK 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35 LSRFAMVALGLITVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crotalus durissus terrificus (South American rattlesnake).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Leduc M., Bon C.;
"Cloning of subunits of convulxin, a collagen-like platelet-
aggregating protein from Crotalus durissus terrificus venom.";
Biochem. J. 333:389-393(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [1] -
SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
TISSUE-Venom gland;
MEDLINE-9832491; PubMed=9657980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 146;
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                                                                                                                                                                                                                                                                                                                                                                                                               16922 MW; 8E1961C59F96757C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 GPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQWICK 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.8%; Score 152.5; DB 1; 24.5%; Pred, No. 3.1e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Convulxin beta precursor (CVX beta).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25; Mismatches
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HSSP, P23807; 11XX.
InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis_ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Viperidae; Crotalinae; Crotalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MGRFIFMSFGFLVVFL---
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146 AA;
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PIR; H29963; WMVZFB.
HSSP; P05140; 2AFP.
InterPro; IRR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
PROSITE; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                     Hypothetical protein; Lectin.
DOMAIN 48 159
     EMBL; D00295; BAA00203.1; -.
                                                                                                                                                                                                                                                           163 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DWNSSLKFCADK--GSHLLTFPDNQG----VKLFGEYLGQDFYWIGLRNI---DGWRWEG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47 TWADAEKFCTQQHTGSHLVSFHSTEEVDFVVKMTHQSLKSTFFWIGANNIWNKCNWQWSD 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MGRFIFVSFGLL-VVFLSL-----SGSEAGFC----CPSHWSSYDRYCYKVFKQEM 46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 LSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-116 FROM N.A.
STRAIN=FP-9 / Isolate HP-438;
MEDLINE=8829622; PubMed=2836548;
MEDLINE=8829622; PubMed=2836548;
"Squence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fowlpox virus (FPV),
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                     INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                      INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20193820; PubMed=10729156; Afonso C.L., Tulman B.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.; "The genome of fcwlpox virus."; The genome of fcwlpox virus."; J. Virol. 74:3815-3831(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of fowlpox virus.";
J. Gen. Virol. 69:1025-1040(1988).
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                   94D7E3E1BC693B9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            V239_FOWPV STANDARD; PRT; 163 AA. P14371; 09J500; 01-JAN-1990 (Rel. 13, Created) 16-CT-2001 (Rel. 40, Last sequence update) 16-CCT-2001 (Rel. 40, Last annotation update) Putative C-type lectin protein FPV239 (BamHI-ORF8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 4.9e-08;
Mismatches 42
                                                                                                                                                                                     CONVULXIN BETA.
                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14.6%; Score 150.5;
                                                                                                                                                                                                                                                                                                                                                                (POTENTIAL)
Pfam; PF00059; lectin_c; 1.
PRINTS; PR01504; PNCREATITSAP.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Lectin; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF198100; AAF44583.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                   17402 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           llarity 31.4%;
Conservative 1
                                                                                                                                                                                148
145
26
                                                                                                                                                                                                                                                                                     38
                                                                                                                                                                                                                                                                                                              144
                                                                                                                                                                                                                                                                                                                                                                                           136
                                                                                                                                                                                                                                                                                                                                                                                                                   148 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 38; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Avipoxvirus.
NCBI_TaxID=10261;
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34
26
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55
100
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                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FPV239.
                                                                                                                                                           SIGNAL
                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       V239 FOWPV
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                                                                                                            3,
                                                                                                                                                                                               100
                                                                                                                                                    73 PSCPILWTRNG----SHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNOGVKLFGEYLG 127
                                                                                                                                                                                                                                        128 ODFYWIGLRNID----GWRWEGGPALSLRILINSLIORCGAIHRNGLOASSCEVALQWICK 184
                                                                                                                                                                                                                                                                   101 PGNHWIGIEKVDFNGTWKLEDGSSYD-NIVPIKGIGDCAYLSDRSIMSSFCFLPKKWICR 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98319530; PubMed=9657448; Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M., Suzuki M., Matsui T., Titani K., Yoshioka A.; "The cDNA cloning and molecular characterization of a snake venom platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon halys bromhoffii venom."; Thromb. Haemost. 79:1199-1207(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thromb. Haemost. 79:1199-1207(1998).
-!- FUNCTION: Binds to platelet glycoprotein Ib and enhances platelet aggregation at low-shear stress. At high-shear stress, aggregation is inhibited.
                                                                                                                                                                                               PDIKILYCKEGWVGYNKNCYFFSEKNNKSLAVERCKDMDGHLTSISSKEEFKFILRYKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., SEQUENCE OF 24-56, SUBUNIT, AND MASS SPECTROMETRY
                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Epidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Gloydius.
                                                                                                            6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: NW=15413; NW_ERR=6; METHOD=Electrospray;
                                                                 Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SUBUNIT: Heterodimer of alpha and beta chains; disulfide-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: Contains 1 C-type lectin family domain.
159 C-TYPE LECTIN.
18635 MW, 5156DC8928855532 CRC64;
                                                               DB 1;
                                                                                                            57;
                                                                 14.2%; Score 146.5; DB 1
26.8%; Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Mamushigin beta chain precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     146 AA.
                                                                                                              24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30; GO:0005576; C:extracellular; IC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB019616; BAA34425.1; -.
                                                                                                            33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P23807; 11XX.
                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RANGE=24-146.
                                                                                                                                                                                                                                                                                                                                185 KVL 187
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DISULFID
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CARBOHYD
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                                                                                                                                                                                                                                                                                      95 DWNSSLKFCAD--KGSHLLTFPDNQG----VKLFGEYLGQDFYWIGLRNIDGW-----RW 143
                                                                                                                                                                                                                                                                                                     45 TWEDAEKFCTQQRKESHLVSFHSSEEVDFVVSMTWPILKYDFVWIGLINII--WNECHVJEW 102
                                                                                                                                                                                                                                                        35 LSRFAMVALGLITVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDILINE=99173880; PubMed=10072769;
Yokoyama-Kobayashi M., Yamaguchi T., Sekine S., Kato S.,
"Selection of CDNAs encoding putative type II membrane proteins on the cell surface from a human full-length cDNA bank.",
                                                                                                                                                                                                                                                                                                                                                                                                                 CLE2_HUMAN STANDARD; PRT; 149 AA.
929478; Q982478; Q902484;
28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-type lectin superfamily member 2 (Activation-induced C-type lectin).
CLESP2 OR AICL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-22388257; PubMed-12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Maruslina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hamann J., Montgomery K.T., Lau S., Kucherlapati R., van Lier R.A.W., "AICL, a new activation induced antigen encoded by the human NK gene
                                                                                                                                                                                                                       Gaps
                                                                                                                                        INTERCHAIN (WITH C-103 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                        48;
                                                                                                                                                                                                 Length 146;
                                                                                                                                                                                                                                                                                                                                                    ----HNAWITESECIAAKTTDNQWLSR 132
                                                                                                                                                                                                                                                                                                                                    144 EGGPALSLRILTNSLIORCGAIHRNGLQASSCEVAL----QWICK 184
                                                                                                                                                                                                                        55; Indels
                                                                                                                                                                          9EDA84BDCC24E76D CRC64;
                                                                                           MAMUSHIGIN BETA CHAIN.
                                                                                                                                                                                                Score 145; DB 1;
Pred. No. 1.7e-07;
                                                                                                                                                  (BY SIMILARITY).

SY SIMILARITY.
                                                                                                      C-TYPE LECTIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                     17; Mismatches
                                                                                                                           SIMILARITY
GO:0007596; P:blood coagulation; IDA
         InterPro; IPR001304; Lectin C.
Pfam; PR0059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
Blood coagulation; Lectin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=97190245; PubMed=9038101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mmunogenetics 45:295-300(1997)
                                                                                                                                                                         17064 MW;
                                                                                                                                                                                               14.18;
27.38;
                                                                                                                                                                                                                     45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Urinary bladder;
                                                                                          146
143
36
142
98
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                                                                                                                                                                        146 AA;
                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                           103 IDGIRLS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                                                                      DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complex."
                                                                                                                                      DISULFID
                                                                                                                                                             DISULFID
                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                               Query Match
                                                                              SIGNAL
                                                                                                      DOMAIN
                                                                                           CHAIN
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                                                                                                                                                                                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 KDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGL---RNIDGWRWEGGPALS 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO:0005530; F:lectīn; TAS. GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 HLSRFAMVALGLITVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEK 93
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.D., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Schorley R.W., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E., Jones S.J.M., Marra M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
tissues,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5 HKKCFIIVGV-LITTVIITLIVKL----TRDSQ----SLCPYDWIGFONKCYYFSKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
                                                                                                                                                                                                                                     Length 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                151 LRILINSLIQR----CGAIHRNGLQASSCEVALQWICKKVLY 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           111 ---FTKSFGMRGSEGCAYLSDDGAATARCYTERKWICRKRIH 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0B4FED23424F6C55 CRC64;
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BY SINILARITY.

BY SINILARITY.

BY SINILARITY.

N-LINKED (GLCNAC. ..) (F

N-Y (IN REF. 3).

D -> H (IN REF. 1).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:2053; CLECSF2.
MIM; 603242; -
GO; GO:0005887; C:integral to plasma membrane; TAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Transmembrane; Lectin; Signal-anchor.
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.0%; Score 144; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AB015628; BAA76495.1; -. EMBL; BC005254; AAH05254.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001304; Lectin_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X96719; CAA65480.1;
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149 AA;
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FOWPV
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                                                                                                                                                                          P14370
                                                                                                                                FOWPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 KWADAERRECTEGRITGAHLVSIESNTEAAFVNQMISENIKKTDYVWIGLTVQNEEQQCKSR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DWNSSLKFCADK--GSHLLTFPDNQGVKLFGEYLGQ-----DFYWIGL--RNIDGW---R 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 LSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MGRFIFVSFGLL-VVFLSL-----SGAEDDS-----DCPSDWSSNGRFCYKLFQQKM 46
                                                                                                                                                                                                                                                                                                          MEDINE=98119530; PubMed=9657448;
MEDINE=98119530; PubMed=9657448;
Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M., Suzuki M., Matsui T., Titani K., Yoshioka A.,
"The cDNA Cloning and molecular characterization of a snake venom platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon halys bromhoffii venom.";
Thromb. Haemost. 79:1199-1207 (1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thromb. Haemost. 79:1199-1207(1998).
-!- FUNCTION: Binds to platelet glycoprotein Ib and enhances platelet aggregation at low-shear stress. At high-shear stress, aggregation is inhibited.
                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A., SEQUENCE OF 22-58, SUBUNIT, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INTERCHAIN (WITH C-98 IN BETA CHAIN) (BY
                                                                                                                                                          Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Gloydius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULLAR LOCATION: Secreted.
MASS SPECTROMETRY: NW-16825; NW_ERR=2.7; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26;
                                     10-0CT-2003 (Rel. 42, Created)
10-0CT-2003 (Rel. 42, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Mamushigin alpha chain precursor.
Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Heterodimer of alpha and beta chains; disulfide-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               51; Indels
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SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                // SIMILARITY.
47DAA17891CE1865 CRC64;
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Pred. No. 7.4e-07;
26; Mismatches 51;
157 AA
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BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00059; lectin_c; 1.
PRINTS; PR01504; PNCREATITSAP.
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26.4%;
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  STANDARD;
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SIGNAL
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Best Local Similarity
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34
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  MIMHA AGKHA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tomley F., Binns M., Campbell J., Boursnell M.E.G.,
"Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           D.L.;
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Afonso C.L., Tulman E.R., Lu Z., Zsak L., Kutish G.F., Rock
"The genome of fowlpox virus.";
J. Virol. 74:381-3831(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 167;
                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Last sequence update)
Se FFBE-2003 (Rel. 41, Last annotation update)
Putative C-type lectin protein FPV008/FPV253 (BamHI-ORF2).
FPV008 AND FPV253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FIRE TO THE OFFICE THE
                                                                                                                                                                                                                      167 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (0
or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gen. Virol. 69:1025-1040(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=88229622; PubMed=2836548;
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143 WEGGPALSLRILTNSLIQRC 162
                                                       107 WSDRSSVSYENLVKPNSKKC 126
                                                                                                                                                                                                                                                                                01-JAN-1990 (Rel. 13, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF198100; AAF44607.1; -. EMBL; AF198100; AAF44608.1; -. PIR; B29963; WMVZF2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isolate HP-438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D00295; BAA00192.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38; Conservative
                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fowlpox virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 167 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Fowlpox virus (FPV)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avipoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=FP-9
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3023
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                                                                     TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA4 TRIAB
P81114;
                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                           15-JUL-1998 (Rel. 36, Last sequence update)
28-FBB-2003 (Rel. 41, Last annotation update)
Rhodocetin alpha subunit.
Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      || |: |: || || || || || : : || :| :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :| |: :|
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBCELLUIAR LOCATION: Secreted.
-!- SUBCELLUIAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: NW=15955.90; MW ERR=1.44; METHOD=Electrospray.
--- SIMILARITY: Contains 1 C-type lectin family domain.
HSSP; P23806; 11XX.
InterPro; IPR001304; Lectin_C.
Pfam; P800039; lectin_c; 1.
PROSITE; P800034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----WIGLR-----NIDGWRWEGGPALSLRILTNSLIQRCGAI-HRNGL---QAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      venom of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  noncovalent interaction between its subunits.";
Biochemistry 38:7584-7593(1999)
-!- FUNCTION: A potent inhibitor of collagen-induced platelet aggregation. Individually, neither subunit inhibits platelet aggregation. Both subunits are essential.
-!- SUBUNIT: Heterodimer of one alpha and one beta subunit held together by noncovalent interactions rather than by intersubunit disulfide bridges.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Calloselasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Buteleostomi;
Lepidosauria, Squamata; Scieroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Crotalus.
NCBI TaxID=8747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1; Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wang R., Kini R.M., Chung M.C.M., "Rhodocetin, a novel platelet aggregation inhibitor from the Calloselasma rhodostoma (Malayan pit viper): synergistic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (LONG FORM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   / SIMILARITY.
386EAC519DFC674D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42;
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CHH-B beta subunit.
Crotalus horridus horridus (Timber rattlesnake).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4e-05
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(Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-TYPE LECTIN (;
BY SIMILARITY,
BY SIMILARITY.
                               133 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 125.5;
Pred. No. 1.4
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                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=99303998; PubMed=10360956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΒY
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                                                                                     (Rel. 36, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15962 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12.2%;
26.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             || ::||
118 DCEEKNVFMCK 128
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13
127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=8717;
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102
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Venom;
                                                                                     15-JUL-1998
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28-FEB-2003
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                                                     P813<u>9</u>7
RHCA AGKRH
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                               HID DESCRIPTION OF STREET AND STR
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Andrews R.K., Kroll M.H., Ward C.M., Rose J.W., Scarborough R.M.,
Smith A.I., Lopez J.A., Berndt M.C.M., Rose J.W., Scarborough R.M.,
Smith A.I., Lopez J.A., Berndt M.C.M.,
The smith A.I. Lopez J.A., Serndt M.G.M.,
The smith A.I. Lopez J.B.,
The smith A.I. Location of alpha and beta subunits, disulfide-linked.
The smith A.I. Contains I C-type lectin family domain.
TherPro; J.PR002353; AntifreezeII.
TherPro; J.PR002353; AntifreezeII.
The smith A.I. Location C. S. Lope L. Lope L. LopezeIII.
TherPro; J.PR002353; AntifreezeII.
TherPro; J.PR002353; AntifreezeII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCADK--GSHLLTFPDNQGVKLFGEYLGQDFYW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  133 IGLRNIDGW-----RWEGGPALSLRILT---NSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates agglutination.
SUBUNIT: Heterotetramer of the subunits 1, 2, 3 and 4,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 CPSDWSSYEGHCYRVFQQEMTWDDAEKFCTQQHTGGHLVSFRSSEEVDFLVSILKFDLFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INTERCHAIN (WITH C-81 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
Alboaggregin A subunit 4.
Trimeresurus albolabris (White-lipped pit viper).
Trimeresurus Acazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea, Viperidae, Crotalinae, Trimeresurus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98189535; PubMed=9531050; Rowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J., Calvete J.J., Niewiarowski S.; "Alboaggregins A and B. Structure and interaction with human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disulfide-linked.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07835BBCB61E9EAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.1%; Score 124.5; DB 1
25.8%; Pred. No. 1.5e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                123 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C-TYPE LECTIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1;
PROSITE; PS50041; C TYPE LECTIN 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    platelets.";
Thromb. Haemost. 79:609-613(1998)
                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00059; lectin c; l. PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13888 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        116
13
115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity
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9

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toxin botrocetin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BOTA BOTJA
                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ritani K.
                                                                                                                                                               DISULFID
                                                                                                                                                                                                                                                 DISULFID
                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BOTA_BOTJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
  SETTTTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce) or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                       75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCAD--KGSHLLTFPDNQG----VKLFGEYLGQ 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      129 DFYWIGLRNIDGW-----RWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQWIC 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLVWIGLSNL - - WNQCNSQWSDGTXLDYKXWREQFECLVSRTTNNEWLSMDCSSTHSFVC 119
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 24-48; 61-68; 108-120; 139-145 AND
                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Crotalus durissus terrificus (South American rattlesnake).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
Viperidae, Crotalinae, Crotalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aggregating protein from Crotalus durissus terrificus venom.";
Biochem. J. 333:389-393(1998).
-!- FUNCTION: Binds to the platelet and collagen receptor,
glycoprotein VI (GPVI).
-!- SUBUNIT: Heterohexamer of three alpha chains and three beta chains; disulfide-linked.
                                                                                                                                                                                                                                                                                                                                                    13;
                                                                                                                                                                                                                                                                                                           DB 1; Length 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Leduc M., Bon C.;
"Cloning of subunits of convulxin, a collagen-like platelet-
                                                                                                                                                                                                                                                                                                                                                  59; Indels
                                                                                                                                                                              C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                D4CFBEE1219C9B1E CRC64;
                                                                                                                                                                                                                                                                                                       ; Score 124.5; DB 1; Pred. No. 1.6e-05; 18; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last amotation update)
Convulxin alpha precursor (CVX alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         158 AA
                                                                                            SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001304; Lectin_C.
InterPro; IPR003990; Pancreatis_ac.
               InterPro; IPR002353; AntifreezeII.
InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Venom gland;
MEDLINE=98324901; PubMed=9657980;
                                                        Pfam; PF00059; lectin c, l. PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                14365 MW;
                                                                                                                                                                                                                                                                                                         12.1%;
25.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; Y16348; CAA76181.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003990; Pancre
Pfam; PF00059; lectin_c; 1.
                                                                                                                                                                                                                                                                                                                          Local Similarity 25.6
nes 31; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                121
13
119
111
                                                                                                                                                                              1 2 2 30 3 30 1 96 1 123 AA;
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HSSP; P23807; 11XX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             E 120
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                                                                                                                                                                                                                       DISULFID
DISULFID
                                                                                                                                                                                                    DISULFID
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                                                                                                                                                                                                                                                                SECUENCE
                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                             Lectin.
                                                                                                                                                                                DOMAIN
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COVXA CRODU

LD 28-FEB-
DT 28-FEB-
                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ONKEKQCSTKWSDGSSVSYDNLLDLYITKCSLLKKETGFRKWFVASCIGKIPFVCK 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -----GWRWEGGPALSIRILINSLIQRCGAIHR-NGLQ---ASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Venom,
MEDLINE=91129280; PubMed=1993206;
Pujimura Y., Titani K., USami Y., Suzuki M., Oyama R., Matsui T.,
Fujimura Y., Titani K., Ruggeri Z.M.;
Fukui H., Sugimoto M., Ruggeri Z.M.;
Tisolation and chemical haracterization of two structurally and
functionally distinct forms of botrocetin, the platelet coagglutinin
isolated from the venom of Bothrops jararaca.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Primary structure of two-chain botrocetin, a von Willebrand factor modulator purified from the venom of Bothrops jararaca.";
Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
                                                                                                                                                                                   C-TYPE LECTIN.
BY SIMILARITY.
SIMILARITY.
INTERCHAIN (WITH C-100 IN BETA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Structural basis of von Willebrand factor activation by the snake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Depidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crocalinae; Bothrops.
NCBI_TaxID=8724;
                                                                                                                                                                                                                                                                                                                                             INTERCHAIN (WITH C-26 IÑ BETA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22118144; PubMed=12121649;
Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
Liddington R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 158;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93157385; PubMed=8430107;
Usami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95 DWNSSLKFCAD--KGSHLLTFPDNQGVKLFGEYLGQDFY-WIGLRNID---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57; Indels
                                                                                                                                                                                                                                                                                                                                                                      (POTENTIAL).
949F9C6D673E2318 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-UTL-1993 (Rel. 26, Last sequence update)
10-GCT-2003 (Rel. 42, Last annotation update)
Botrocetin, alpha chain (Platelet coagglutinin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                   11.7%; Score 120.5; DB 1
25.0%; Pred. No. 5.3e-05;
PRINTS; PRULDOC, CLECT; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 133 AA.
                                                                                                                                                                                                                                                                                                                  BY SIMILARITY
                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochemistry 30:1957-1964(1991).
                                                                                                                                                                                                                                                                                                                                                                                                  158 AA; 18141 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                :| : || : || : | 47 NWEDAEWFCTKQAKGAHLVS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bothrops jararaca (Jararaca).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity 25.0%
nes 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                 23
158
153
152
104
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                                                                                                                                                          24
34
27
55
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158
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7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 CPSGWSSYEGNCYKFFQQKMMWADAERFCSEQAKGGHLVS-----IKIYSKEKDFVGDL 55
Structure 10:943-950(2002).

-!- FUNCTION: Two-chain botrocetin forms an activated complex with vWF, and the complex then binds to platelet GPID, resulting in platelet agglutination.

CC -!- FUNCTION: There are two distinct forms of the von Willebrand factor-dependent platelet coagglutinin. The dimeric form is determined to platelets of a submitted in promoting vWF binding to platelets.

CC -!- SUBGNIT: Disulfide-linked dimer of an alpha and a beta chain.

CC -!- SUBGNIT: Disulfide-linked dimer of an alpha and a beta chain.

CC -!- SUBGNIT: Disulfide-linked dimer of an alpha and a beta chain.

CC -!- SUBGNIT: Disulfide-linked dimer of an alpha and a beta chain.

CC -!- SUBGNIT: Disulfide-linked dimer of an alpha and a beta chain.

CC -!- SUBGNIT: Disulfide-linked dimer of an alpha and a beta chain.

CC -!- SUBGNIT: Disulfide-linked dimer of an alpha and a beta chain.

CC -!- SUBGNIT: Contains 1 C-type lectin family domain.

PIR, A47267;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     56 VTKNIQSSDLYAWIGLRVENKEKQCSSEWSDGSSVSYENVVERTVKKCFALEKD 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              128 -----QDFY-WIGLR--NID---GWRWEGGPALSLRILTNSLIQRCGAIHRN 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INTERCHAIN (WITH C-75 IN BETA CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 11.6%; Score 119; DB 1; Length 133; 1 Similarity 25.4%; Pred. No. 6.2e-05; 29; Conservative 26; Mismatches 33; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 AA; 15215 MW; E4CF4502946AC74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lectin; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
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Search completed: August 10, 2004, 16:42:47 Job time : 9 secs

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GenCore version 5.1.6
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protein search, using sw model OM protein August 10, 2004, 16:39:05; Search time 32 Seconds (without alignments) 1853.669 Million cell updates/sec Run on:

US-09-811-367B-3

1029 1 MADSSIXSTLELPEAPQVQD......GLQASSCEVALQWICKKVLY 188 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1017041 seqs, 315518202 residues Searched:

396094

Minimum DB seq length: 0 Maximum DB seq length: 188

Total number of hits satisfying chosen parameters:

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

SPTREMBL 25:* Database

sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_mhc:* vertebrate:* unclassified:* sp_bacteria:*
sp_fungi:*
sp_human:* sp_rodent:*
sp_virus:* sp_archea:* sp plant: * Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_bacteriap:*

rvirus:*

sp_archeap:*

		Description	O88713 mus musculu	Q64335 rattus norv	054708 mus musculu	O54707 mus musculu	O8mhy8 pongo pygma	Osmiia pongo pygma	O8mhy9 pongo pygma	OBmii4 pongo pygma	O9nzsl homo sapien	Osspx0 sus scrofa	O9r007 mus musculu	Q9iam0 aqkistrodon	08jiw1 aqkistrodon	095194 bos taurus	Ogalf4 sus scrofa	Q8r4k5 rattus norv
SUMMARIES		ID	088713	064335	054708	054707	Q8MHY8	QBMJI3	6AHM8Ö	Q8MJI4	O9NZS1	OSSEXO	Q9R007	Q91AM0	QSJIWI	Q95JG4	Q9GLF4	Q8R4K5
		DB	11	11	11	11	9	9	9	9	4	9	11	13	13	9	9	11
		Query Match Length DB	188	188	179	179	179	179	179	179	181	159	165	146	146	161	165	132
	₩	Query Match	100.0	81.4	17.5	17.5	17.2	17.0	17.0	16.7	16.7	16.4	16.3	15.9	15.9	15.8	15.6	15.5
		Score	1029	838	180	180	177.5	174.5	174.5	171.5	171.5	169	168	163.5	163.5	163	191	159.5
		Result No.	П	7	m	4	S	9	7	80	6	10	11	12	13	14	15	16

MGD; MGI:1355294; Klrgl.

164 11 QBBL24 165 13 QBAYA4 163 13 QBAY98 179 11 Q35778 185 6 Q9GLF3 185 6 Q9GLF3 186 13 Q9TGF 146 13 Q9TGF 146 13 Q9TG7 149 13 Q9TG7 162 6 QBMT4 162 6 QBMT4 163 13 Q9TG7 164 13 Q9TG7 165 13 Q9TG7 167 14 Q9TC7 183 6 Q9TG7 183 6 Q9TG7 184 13 Q9TC7 187 4 Q9TC7 187 4 Q9TC7 188 13 Q9TC7 189 14 Q9TC7 189 15 Q9TC7 189 16 Q9TC7 189 17 Q9TC7 189 19	Q8b124 mus musculu Q8aya4 agkistrodon Q9gk90 macaca mula Q8av98 trimeresuru Q35778 rattus norv	28jgf6 trimeresuru Q8wup7 homo sapien Q9i840 agkistrodon Q7t045 vipera lebe	Usinzje macaca muja QBmhy4 pongo pygma Q9hd37 homo sapien Q9dg31 agkistrodon Q8uyc7 agkistrodon	Q9ny25 homo sapien Q8ay3 agkistrodon Q9deal agkistrodon Q9ygn4 agkistrodon Q8mjh4 pongo pygma Q8mjh3 pongo pygma	Q95j54 pan troglod Q8j1v7 agkistrodon Q9ukq0 homo sapien Q8uvc6 agkistrodon Q8aya5 agkistrodon Q9def8 agkistrodon Q9def8 agkistrodon Q8cj86 mus musculu
	Q8BL24 Q8AYA4 Q9GK90 Q8AV98 O35778	Q8UGT6 Q8WUP7 Q91840 Q7T045		0 00	$\alpha \alpha$
	164 11 146 13 163 6 148 13 179 11			,	
	15.5 15.4 15.2 15.0 14.9	4.4.4.4.6	44444		<i>.</i>
23 23 24 24 24 24 24 24 24 24 24 24 24 24 24	159.5 156.5 156 154 153	148.5 148.5 146.5 146.5	145 145 145 144 144	143.5 141.5 140.5 139	138.5 137.5 136.5 136.5 136.5 135.5
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ALIGNMENTS

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SEQUENCE FROM N.A.
STRAIN=C.B-17 SCID;
MEDLINE=C.B-17 SCID;
MEDLINE=9907194; PubMed=9862378;
Hanke T., Corral L., Vance R.E., Raulet D.H.;
"2Fl antigen, the mouse homolog of the rat '$1', is a lectin-like type
"2Fl antigen, the mouse homolog of the rat '$1', is a lectin-like type
"I transmembrane receptor expressed by natural killer cells.";
Eur. J. Immunol. 28:4409-4417(1998).
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STRAIN=129/SvevThCfBr; TISSUB=Spleen;
MEDLINE=2111316; PubMed=11220622;
Voebringer D., Kaufmann M., Pircher H.;
"Genomic structure, alternative splicing, and physical mapping of the killer call lectin-like receptor G1 gene (KLRG1), the mouse homologue
                                                                                                                                                                                                                      01-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-607-2003 (TrEMBLrel. 25, Last annotation update)
Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-like receptor 01).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Blaser C.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                             188 AA.
                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, Created)
                                                                                             PRT;
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EMBL, AR097357, AAD03718.1; -.
EMBL, AJ010751, CAR09342.1; -.
EMBL, AF317727; AAX40082.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 2-188 FROM N.A.
                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                  KLRG1 OR MAFA.
Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090;
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RESULT 1
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121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTWSLIQRCGAIHRNGLQASSCEVALQ 180
                                                                                                                                           CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
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                                                                                                                                                                         61 CCGSKGFMCSQCSRCFNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN
                                                                                                                                                                                                                                                                                      1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 SRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRILCCGSKDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=99124458; PubMed=9464811;
Vance R.E., Tanamachi D.M., Hanke T., Raulet D.H.;
"Cloning of a mouse homolog of CD94 extends the family lectins on murine natural killer cells.";
Eur. J. Immnol. 27:3236-3241(1997).
EMBL, AF030312; AAC28244.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20809 MW; D59E1CBB63139E45 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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Last sequence update)
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SMARY; SM0034; CLECT; l.
PROSITE; PS50041; C_TYPE_LECTIN_2; l.
PROSITE; PS00022; EGF l; l.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1196275; Klrdl.
GO; GO:0005259; R:sugar binding; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR001304; Lectin_C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLRD1 OR CD94
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01-JUN-1998
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Guthmann M.D., Tal M., Pecht I.;
"A secretion inhibitory signal transduction molecule on mast cells is another C type lectin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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80.7%; Pred. No. 1.5e-79;
ive 15; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                            Indels
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STRAIN-SPRAGUE DAWLEY; TISSUB=Testis;
STRAIN-SPRAGUE DAWLEY; TISSUB=Testis;
BOOCK Jr P., Guthmann M.D., Pecht I.;
Submitted (APR-1996) to the BMBL/GenBank/DDBJ databases.
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188 AA; 21356 MW; 2CC8032D4D020B15 CRC64;
                                                                                                                                                                                                                              188 AA; 21396 MW; 876336802EA134F1 CRC64;
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Last annotation update)
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005259; F:sugar binding; IEA.
GO; GO:000157; P:heterophilic cell adhesion; IEA.
InterPro; IPR01304; Lectin_C;
FAM, PF00059; lectin_C; 1...
FAMARY; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_Z; 1.
                                                                                                                                                                                                                                                                                   100.0%; Score 1029; DB 11;
100.0%; Pred. No. 1.5e-99;
iive 0; Mismatches 0;
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EMBL; X97191; CAA65829.1; -.
EMBL; X97192; CAA65829.1; JOINED.
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EMBL; X97194; CAA65829.1; JOINED.
EMBL; X97195; CAA65829.1; JOINED.
EMBL; X79112; CAA56208.1; -.
PIR; IS9421; IS9421.
GO; GO:0005529; F:sugar binding; IEA.
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Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
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Best Local Similarity 80.75
Matches 151; Conservative
                                                                                                                                                                                                                                                                                                                                            188; Conservative
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                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                                                                                   Lectin; Receptor.
SEQUENCE 188 A
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SEQUENCE
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                                                                                                                                                                                                                                                                                      Query Match
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9

Gaps

DAY REPARENCE OF THE PARENCE OF THE

62

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01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
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                                                                                                                            J. Immunol. 169:220-229(2002).
EMBL; AF470381; AAM78481.1; -.
EMBL; AF470382; AAM78482.1; -.
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Best Local Similarity
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SEQUENCE
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Best Local 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 DKWVGHQCNCYFISKEEKSWKRSRDFCASQNSSLLQ-PQSRNELSFWNF-SQTFFWIGMH 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----CSHCPSCP 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRWRLMSVIPGIK-CLFLMVTLG---VLLINSFTIQNIQSTPSPTTVVEFQEVSECCVCL
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                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CS7BL/61; TISSUE=Mammary gland;
Butcher S., Cottage A., Cook G.P.;
"Mouse natural killer cell receptors homologous to human CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Pongo.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Killer cell lectin-like receptor, subfamily D, member 1 (CD94).
                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=CS7BL/6J;
Heusel J.W., Ho E.L., Brown M.G., Matsumoto K., Yokoyama W.M.;
"Murine CD94.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Score 180; DB 11; Length 1; Pred. No. 9.2e-11; 25; Mismatches 75; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 AA; 20808 MW; DD343419E93B3465 CRC64;
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(TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                              Vance R.E., Tanamachi D.M., Hanke T., Raulet D.H.;
Eur. J. Immunol. 27:0-0(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MGD; MGI:1196275; Klrdl.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
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InterPro; IPR001304; Lectin C.
Pfam; PF000059; lectin c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS000022; EGF 1; 1.
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SEQUENCE FROM N.A.
MEDLINE=22072192; PubMed=12077248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF030311; AAC28243.1; -. EMBL; AF057714; AAC33713.1; -. EMBL; AF039025; AAD02116.1; -.
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31.8%;
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                                                                                               Mus musculus (Mouse).
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                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                  STRAIN=C57BL/6;
                                                               OR CD94.
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                                                               KLRD1
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MEDLINE-22072192; PubMed=12077248;
MEDLINE-22072192; PubMed=12077248;
Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
T. Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
T. Mik Cell Receptors of the Oranguan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors of Limmunol. 169:220-229(2002).
T. Immunol. 169:220-229(2002).
T. EMBL; AR470384; AAM78484.1; -..
M. GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005529; F:receptor activity; IEA.
M. InterPro; IPR001304; LecTin.C.
M. Fram; PR00059; LecTin.C.
M. Fram; PR000059; LecTin.C.
M. Fram; PR00039; CIRCT; 1.
M. PROSITE; PS00041; CIYPE LECTIN.Z; 1.
M. PROSITE; PS00022; EGF_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                85 HCYYPSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71 NCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEEHTAW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              84
Guethlein L.A., Flodin L.R., Adams E.J., Parham P.; "NK Cell Receptors of the Oranguean (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C.";
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              142 RWEGGPALS --- LRILTNSLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        129 LWENGSALSQYLFPLFETFNPKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17.2%; Score 177.5; DB 6; Length 179; ilarity 31.8%; Pred. No. 1.7e-10; Conservative 16; Mismatches 69; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 179;
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Last annotation update)
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31.2%; Pred. No. 3.4e-10;
tive 17; Mismatches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ā
                                                                                                                                                                                                                                                GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005529; F:receptor activity; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_C; 1.
SMART; SMORD34; CLECT; 1.
PROSITE; PS50041; C TECT; 1.
PROSITE; PS00022; EGF_1; 1.
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RESULT 7

OBMHY9

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14 GTIGIICLSITATLGILLKNSFTKLSIEPAFTPGPDIELQKDSDC--C-SCQEKWVGYRC 70
                                                                           SEQUENCE FROM N.A.
MEDLINE=22072192; PubMed=12077248;
Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;
Guethlein Lo.A., Flodin L.R., Adams E.J., Parham P.;
NK Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal
Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
with MHC-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THUMAIN KLRET, a novel member of the killer cell lectin-like receptor gene family: molecular characterization, genomic structure, physical mapping to the NK gene complex and expression analysis.";

Bur. J. Immunol. 30:568-576(2000).

EMBL; AF15207; AAF37805.1; -.

GO; GO:001602; Camedrane; TAS.

GO; GO:0030106; F:MHC class I receptor activity; TAS.

Fran, PRO035; Lectin.C.

Fran, PRO035; Lectin.C.

PROSITE; PS50041; CLECT; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20135860; PubMed=10671213;
Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
Fernandez-Ruiz E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
Craniata, Vertebrata, Euteleostomi;
Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         142 RWEGGPALS --- LRILINSLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129 LWENGSSLSQYLFPLFETFNPKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 4; Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 6; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                             674489E5EC6F8780 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21204 MW; 64642240CAE1E551 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-JUN-2003 (TrEMBLrel. 15, Last sequence update) Lectin-like receptor F1, splice variant 1 KLRF1-s1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 16.7%; Score 171.5; DB 6;
31.2%; Pred. No. 7.1e-10;
Live 16; Mismatches 70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ā
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                                                                                                                                                                                             44 GLLTVILMSLLMYQRILCCGS------
                                                                                                                                                                                                                                                                                                             Pfam; PF00059; lectin c; 1.
SMART; SM00034; CLET; 1.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
PROSITE; PS00022; EGF 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 15, Created)
(TrEMBLrel. 15, Last seq
(TrEMBLrel. 24, Last ann
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Chordata; (Primates; (
                                                                                                                                                                                                                                                                                                                                                                                                               179 AA; 20536 MW;
                                                                                                                                                                                                                                                                        InterPro; IPR006209; EGF like InterPro; IPR001304; Lectin_C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16.78;
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nes 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
    Eukaryota; Metazoa;
                      Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 AA;
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                    Mammalia, Euther
NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI TaxID=9606;
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01-OCT-2000 (
01-JUN-2003 (
                                                                                                                                                                                                                                                                                                                                                                                                Receptor.
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SEQUENCE
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Matches
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                                                                                   85 HCYYPSMEKKDWNSSLKFCADKGSHLLTFPDNOGVKLFGEYLGODFYWIGLRNID---GW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GTLGIİCLSLTATLGİLIKNSFTKLSIEPAFTPGPDIELQKDSDC--C-SCQEKMVGYRC 70
                    70
  MEDLINE=22072192; PubMed=12077248; Guethlein L.A., Flodin L.R., Adams E.J., Parham P.; UNK Cell Receptors of the Grangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C.";
                                                           HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                             Pongo pygmaeus (Orangutan).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 LWENGSALSQYLFFLFFTFNPKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 RWEGGPALS---LRILTNSLIORCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                        142 RWEGGPALS---LRILTNSLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                             129 LWENGSSLSQYLFPLFFTFNPKNCIAYNPNGNALDESCEDKNRYLCKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 17.0%; Score 174.5; DB 6; Length 179; Sest Local Similarity 31.8%; Pred. No. 3.4e-10; Aatches 54; Conservative 15; Mismatches 70; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    179 AA; 20520 MW; 674489E5FBD95CFA CRC64;
                                                                                                                                                                                                                                                                                                             01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-0CT-2002 (TrEMBLrel. 22, Created)
01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Natural viller cell receptor.
POPY-CD94.
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BMBL, AP470380; AAM78480.1; --
BMBL, AP470380; AAM78480.1; --
GO, GO:0004872; F:receptor activity; IEP
GO, GO:0005529; F:sugar binding; IEA.
InterPro: IPR006209; EGF like.
InterPro: IPR001304; Lectin_C.
Pfam; PF00059; lectin_C; l.
PROSITE; PS00041; C_TYPE_LECTIN_2; l.
PROSITE; PS00042; EGF_L; l.
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                                                                                                                                                                                                                                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                          Natural killer cell receptor.
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                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                              POPY-CD94.
                                                                                               7.7
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Q8MJ14 Q8MJ14;

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RESULT 8 Q8MJ14

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ransmembrane.
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                                                                                                                                                                                                                                                                                        SEQUENCE
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Matches
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                                           44 GLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFC 103
                                                                                        104 ADKGSHILITEPDNQGVKLFGEYLGQ-DFYWIGLRNID----GWRWEGGPALSLRIL---- 154
                                                                                                         71 HCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCA-DKGSHLLTFPDNQGVKLFGEYLGQD 129
                                                         HVSSCPDDWIGYQTKCYFISKKTKNWTLAQSFCSKHHGATLALLESKEDMVFLKQHVGRA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 FYWIGLRNIDG--WRWEGGPALSIRI-LINSLIQRCGAIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                   Yim D., Sotiriadis J., Kim K.-S., Shin S.-C., Jie H.-B.,
Rothschild M.F., Kim Y.B.;
"Molecular cloning, expression pattern, and chromosomal mapping of pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; MusinCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                      31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.4%; Score 169; DB 6; Length 15
30.3%; Pred. No. 1.1e-09;
ive 22; Mismatches 55; Indels
                     53; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF484234; AAL91547.1; -. GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectir_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 159 AA; 18056 MW; Ä19C3EEBAE92AA69 CRC64;
                                                                                                                                                                                                                                                          01-JUN-2002 (TrEMBLrel. 21, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Type II membrane protein CD69 splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-CT-2003 (TrEMBLrel. 25, Last annotation update)
Type II transmembrane protein MDL-1 (C-type).
        Pred. No. 7.2e-10;
                                                                                                                                        155 -- TINSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                      159 AA.
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                      Mismatches
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STRAIN-BALB/C; TISSUE-Myeloid;
MEDLINE=99380598; PubMed=10449773;
27.6%; Fir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Conservative
                     42; Conservative
                                                                                                                                                                                                                          PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
          Similarity
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                scrofa (Pig)
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          Best Local
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                     Matches
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SMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG---WRWEGG 146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40 MVALGLLTVIL-----MSLLMYQRILCCGSKDS----TCSHCPSCPILWTRNGSHCYYF 89
                                                                                                                                                                                                      the RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-langth cDNAs.";
Nature 420:563-573(2002).

EMBL; AF139769; AAF02492.1;
EMBL; AR139769; BAC29537.1;
EMBL; AR036697; BAC29537.1;
EMBL; GO, GO:00160215; Clausers Lto membrane; IEA.

GO, GO:0016021; C:integral to membrane; IEA.

GO, GO:0016021; Lectin. C.
Bakker A.B., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.; "Myeloid DAPL-associating lectin (MDL)-1 is a cell surface receptor into activation of myeloid cells.", Proc. Natl. Acad. Sci. U.S.A. 96:9792-9796(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Agkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus). Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Agkisacutacin, a new fibrinolytic & anti-platelet protein from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cheng X., Qian Y., Liu Q., Li B.X.Y., Ding J., Xu Z., Huang W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.3%; Score 168; DB 11; Length 165; 28.4%; Pred. No. 1.5e-09; Live 25; Mismatches 69; Indels 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agkistrodon acutus venom.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             147 PALSLRILTNSLIQRCGAIHRNGL----QASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              123 SVFNGNVTNODONFDCVTI---GLTKTYDAASCEVSYRWICE 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 AA; 19055 MW; 626D64392A513282 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    146 AA
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GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001304; Lectin_C.
InterPro; IPR001399; Pancreatis_ac.
Pfam; PP00059; lectin_c; 1.
SMART; SR01054; PNREATITSAP.
SMART; R000014; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last seq
01-0CT-2003 (TrEMBLrel. 25, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                      STRAIN=C57BL/6J; TISSUB=Bone; MEDLINE=22354683; PubMed=12466851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF176421; AAF26287.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00059; lectin_c; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                     The FANTOM Consortium,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SM00034; CLECT
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tes 46; Conserv
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SEQUENCE FROM N.A.
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100 WIGLNFTLSGKSWKWINGSFLNSNILPIFGDAKEDCCVYISKTQCISDYCAAKNRWICQK 159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 132 WIGLR-NIDG--WRWEGGPALSLRILT---NSLIQRCGAIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 TCPMHWKRIRDKCLYFSETSKPWNDSLADCSTRESSLLLIQDQEELRLMQNLINKEGILF 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21308528; PubMed=11414735;
Yim D., Jie H.B., Sotiriadis J., Kim Y.S., Kim Y.B.;
"Molecular cloning and expression pattern of porcine myeloid DAP12-
                                   Bos taurus (Bovine).
Bukaryota; Metazooa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sus scrofa (Pig).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                Govaerts M.M., Goddeeris B.M.; "Homologues of natural killer cell receptors NKG2-D and NKR-P1
Natural killer cell receptor protein 1 variant 1 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165 AA; 18653 MW; 40C29ABE136E76D3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     24F9AA44A19EAFB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Tremblrel. 16, Created)
(Tremblrel. 16, Last sequence update)
(Tremblrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    associating lectin-1.";

Cell. Immunol. 209:42-48(2001).

EMBL; AF285449; AAG29427.1; -.

GO; GO:0005529; F:sugar binding; IEA.

GO; GO:0007157; P:heterophilic cell adhesion; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.8%; Score 163; DB 6; 31.1%; Pred. No. 4.9e-09; iive 20; Mismatches 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myeloid DAP12-associating lectin short form.
                                                                                                                                                                                                                                                     Immunopathol. 80:339-344 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165 AA
                                                                                                                                                                                                                                                     InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; R000034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                            PROSITE, PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                TISSUE=Spleen;
MEDLINE=21351526; PubMed=11457486;
                                                                                                                                                                                                                                                                                                                                                                                                                             161
\: 18648 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 31.1<sup>§</sup>
Matches 38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                      expressed in cattle.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 AA;
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                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                    161
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SEQUENCE
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Q9GLF4
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                                                                                                                                                                                 DWNSSLKFCAD--KGSHLLTFPDNOG----VKLFGEYLGQDFYWIGLRNI-DG--WRWEG 145
                                                                                                                                                                                                                     45 TWADAEKFCTQQHKGSHLASFHSSEEADFVVTLTTPSLKTDLVWIGLKNIWNGCYWKWSD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    45 TWADARKFCTQQHKGSHLASFHSSEEADFVVTLTTPSLKTDLVWIGLKNIWNGCYWKWSD 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 LSRFAMVALGLLTVILMSLLMYQRILCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK
                                                                                                          35 LSRFAMVALGLLTVILMSLLMYQRILCCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKK
                                                                                                                                              MGRFIFVSFGLLVVFL-----SLSGTAADCPSD---WSSYEGHCYKPFDEPK
                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ağkistrodon acutus (Hundred-pace snake) (Deinagkistrodon acutus). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosuuria; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Croalinae; Deinagkistrodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25;
                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15.9%; Score 163.5; DB 13; Length 146; 30.2%; Pred. No. 3.9e-09;
                                       DB 13; Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71; Indels
                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu H., Xiang K., Wang Y., Liu J.;
"B chain of agkisacutacin from Deinagkistrodon acutus.";
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AY091756, AAM22785.1;
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PIR, JC7135, JC7135.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; JC7135; JC7135.

GO; GO: 0005229; F: sugar binding; IEA.

InterPro; IPR001304; Lectin C.

InterPro; IPR003990; Pancreatis ac.

Ffam; PR00059; lectin c; 1.

PRINTS; PR01504; PRCEEDITSAP.

SMART; SM0004; CLRCT; 1.

PROSITE; PS00615; C TYPE LECTIN 1; 1.

PROSITE; PS50041; C TYPE LECTIN 1; 1.

PROSITE; PS50041; C TYPE LECTIN 2; 1.
   7360B6D6864131BB CRC64;
                                                                                                                                                                                                                                                        GPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                        GIKLDYKDWREQFECLVSRTVNNEWLSMDCGTTCSFVCK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      146 GPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105 GTKLDYKDWREQFECLVSRTVNNEWLSMDCGTTCSFVCK 143
                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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Last annotation update)
                                   15.9%; Score 163.5; DB 13; 30.2%; Pred. No. 3.9e-09; tive 15; Mismatches 71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 AA
                                                                                                                                                                                                                                                                                                                                                                                146 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
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   16726 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19,
01-DEC-2001 (TrEMBLrel. 19,
01-OCT-2003 (TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                  22,
22,
25,
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                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002 (TrEMBLrel. 01-OCT-2003 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Aqkisacutacin B-chain.
     146 AA;
                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
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01-0CT-2002
                                                                          48;
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   SEQUENCE
                                   Query Match
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Q95JG4;
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Matches
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SO ON BREAT

095JG4

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8; Gaps

56; Indels

Length 161;

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7;
                                                      Query Match 15.6%; Score 161; DB 6; Length 165;
Best Local Similarity 29.1%; Pred. No. 8.1e-09;
Matches 48; Conservative 25; Mismatches 66; Indels 26; Gaps
                                                        Sy da
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88 YFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG---WRWE 144

ð

Search completed: August 10, 2004, 16:44:03 Job time : 33 secs

⁶¹ FLSTSENSWNNSMNFCKQKGSTLAIVNTPEKLKFLQNISGAEKYFIGLLYQPAEKMWRWI 120

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GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

- protein search, using sw model OM protein August 10, 2004, 16:35:35; Search time 47.5 Seconds (without alignments) 1118.293 Million cell updates/sec Run on:

US-09-811-367B-3

1 MADSSIYSTLELPEAPQVQD......GLQASSCEVALQWICKKVLY 188 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

1586107 seqs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

1082526

Minimum DB seq length: 0 Maximum DB seq length: 188

Listing first 45 summaries Post-processing: Minimum Match 0% Maximum Match 100%

geneseqp2001s:* geneseqp2002s:* geneseqp2003as:* geneseqp2003bs:* A_Geneseq_29Jan04:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2004s;* 7::9 Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	Aael1760 Mouse mas	e		Rat	Part		Human	CD94.		6 Human		Human		Human	Human	Human	Human	3 Human		Aau19816 Human nov	Human	Human	Human	Human	Human
SUMMARIES		AAE11760	AAR77033	AAW88277	AAE11761	AAR77472	AAW88267	AAW64791	AAW40222	ADE76965	AAM80296	ABG72616	AAM80302	AAW27288	ADC38664	AAU19660	ABP47880	ADC10842	AAU00673	AB032541	AAU19816	ABP48036	ADC10998	AAU19836	AAU19690	ABB15422
	DB	4	C1	N	4	7	7	7	7	œ	4	9	4	7	7	4	Ŋ	7	4	9	4	2	7	4	4	4
	Length		188		18	11	66	17	179	179	142	142	160	181	181	182	182	182	165	165	94	94	94	140	140	140
٥¥	ਨੂਪ	100.0	81.4	81.4	81.4	53.5	21.6	17.3	17.3	17.3	16.3	16.3	16.3	15.6	15.6	15.2	15.2	15.2	15.0	15.0	14.4	14.4	14.4	14.4	14.4	14.4
	Score	1029	838	838	838	ſΩ	222.5	178.5	178.5	178.5	167.5	167.5	167.5	9	160.5	156	156	156	154	Н	148.5	148.5	148.5	148.5	48.	148.5
	Result No.		7	m	4	ហ	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25

Abb17909 Human ner Abp48056 Human pol Abp47910 Human pol Adc10872 Human ext		Abb33139 Peptide # Aam26602 Peptide # Abb27967 Human pep	Abb18604 Protein # Aam66323 Human bon Aam53935 Human bra		Human Secret Human	DITOR
ABB17909 ABP48056 ABP47910 ADC10872	ADC11018 AAW36957 AAM14192	ABB33139 AAM26602 ABB27967	ABB18604 AAM66323 AAM53935	ABG47989 AAM01928 ABG35971	AAU00675 ABO32547 AAM25760 AAM51544	1
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4444	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	1 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	14.3 14.3	14.3 14.3	4 4 4 4 4 4 4 4 1 1 1 1 1 1 1 1 1 1 1 1	
148.5 148.5 148.5	148.5 148 147	147 147 147	147 147 147	147 147 147	145 145 145 145 155	
7 7 7 9 7 9	332	33.4 35.4 35.4	36 38 38	39 41 41	4 4 4 4 2 6 4 0	

ALIGNMENTS

Mouse; pharmaceutical composition; mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic, Mouse mast cell function associated antigen (MAFA) protein. AAE11760 standard; protein; 188 AA. (first entry) 18-DEC-2001 AAE11760;

Mus sp

64. .188 /note= "Extracellular domain" Location/Qualifiers 64. .188 Domain

WO200170805-A2

27-SEP-2001

16-MAR-2001; 2001WO-US008596.

17-MAR-2000; 2000US-0190716P

(GEMI-) GEMINI SCI INC.

.. Takahashi N, Mikayama

WPI; 2001-611482/70. N-PSDB; AAD18735.

Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.

Example 1; Page 19; 49pp; English.

The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (WAFA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MAFA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAFA binding to a ligand on a target cell, by contacting the pharmaceutical

combination with the MAFA to prevent inflammatory and allergic reactions

Sequence 188 AA;

S X S

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composition in vitro, ex vivo or in vivo by administering the composition an amount sufficient to inhibit cell surface MRFA binding to the ligand on the target cell. The agent or the composition is useful for treating a tummour by stimulating the cytotoxic activity of an NK cell or a cytotoxic activity of an NK cell or a cytotoxic tummour cell. The invention is also useful for inhibiting an activity of NK cell or a cytotoxic activity of an NK cell or a cytotoxic tummour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell craw.
                                                                                                                                                                                                                                                                  120
                                                                                                                                                                                                                                                                                            120
                                                                                                                                                                                                                                                                                                                                                  180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mast cell function-associated antigen; MAFA; soluble; ligand; identification; screening; inflammation; inflammatory; allergic;
                                                                                                                                                                                                                                                                                                                        LFGEYLGODFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel DNA encoding a mast cell function-associated antigen (MAFA) - useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions.
                                                                                                                                                                                                             9
                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                         1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLITVILMSVLLMYQRIL
                                                                                                                                                                                                                                                                                    1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                                                                                                  CCGSXDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK
                                                                                                                                                                                   Gaps
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0
                                                                                                                                                         Length 188;
                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalian mast cell function-associated antigen (MAFA)
                                                                                                                                                       100.0%; Score 1029; DB 4;
100.0%; Pred. No. 6.6e-103;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR77033 standard; protein; 188 AA.
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                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                    WICKKULY 188
                                                                                                                                                                                                                                                                                                                                                                                WICKKULY 188
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                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAT01471
                                                                                                                               Sequence 188 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (YEDA ) YEDA R
(RYCU/) RYCUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rattus rattus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   prevention
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                                                                                                                                                                                                                                                                                                                         121
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A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in

Claim 12; Page 37; 54pp; English.

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                                                                                                          CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                            61 CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                             This is the amino acid sequence of rat mast cell function-associated antigen (MAFA), a type II membrane glycoprotein found on mast cells and basophils. The invention relates to cloning of the human MAFA molecule (see AAW88265) and to the discovery of splice variants (see AAW88266-67) of human MAFA that are not found in rat. Polypeptides and synthetic
                                                     09
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                                                                     1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILINSLIQRCGAIHRNGLQASSCEVALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy.
                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                              Mast cell function-associated antigen; MAFA; splice variant; rat; inflammation; allergy; asthma; rheumatoid arthritis; tumour; ther
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0
                          21; Indels
Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lamont A, Williams DH;
                                                                                                                                                                                                                                                                                                                                                                                                      Rat mast cell function-associated antigen (MAFA)
81.4%; Score 838; DB 2;
80.7%; Pred. No. 3.2e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12. .84
'note= "Asn is N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97. .99
/note= "Asn is N-glycosylated"
                           15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        AAW88277 standard; protein; 188 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 4; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PEPT-) PEPTIDE THERAPEUTICS LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-GB001572,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases, and tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lamers MBAC,
                            151; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1999-059806/05.
N-PSDB; AAV84222.
                                                                                                                                                                                                                        WICKKVL 187
                                                                                                                                                                                                                                                  WICEKVL 187
               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
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  Query Match
Best Local
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                                                                                                                                                                                                                         CGGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLIFFPDNQGVN 120
                                                                                                                                                                                                                                                             LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180
                                                                                                                                                                                                                                                                           1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL 60
                                                                                                                                                                   peptides (see AAW88258-64) based on human MAFA and human truncated MAFA, and polymucleotides encoding them, can be used in methods for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), and tumour growth
                                                                                                                             Gaps
                                                                                                                             ..
                                                                                                 Length 188;
                                                                                                                           21; Indels
                                                                                               ; Score 838; DB 2;
; Pred. No. 3.2e-82;
15; Mismatches 21
                                                                                                 81.4%;
                                                                                                           80.7%;
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                   WICKKVL 187
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WICEKUL 187
                                                                                                           Similarity
                                                                      AA;
                                                                    Sequence 188
                                                                                                                         151;
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                                                                                              Query Match
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Rat mast cell function associated antigen (MAFA) protein. AAE11761 standard; protein; 188 (first entry) 18-DEC-2001 AAE11761; AAE1176 RESULT

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mast cell function associated antigen; composition; mast cell function associated antigen r cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic Rat; pharmaceutical c MAFA; natural killer

Rattus norvegicus.

WO200170805-A2.

27-SEP-2001

16-MAR-2001; 2001WO-US008596.

17-MAR-2000; 2000US-0190716P

(GEMI-) GEMINI

Mikayama rakahashi N,

2001-611482/70. N-PSDB; AAD18736 irmaceutical composition for treating tumor by stimulating cytotoxic sivity of natural killer cell or T-cell, comprises an agent that binds mast cell function-associated antigen ligand on target cell. Pharmaceutical compactivity of natural

Example 1; Page 19; 49pp; English.

The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MAPA) ligand on a target cell, and prevents or inhibits natural killer (NK) or T-cell-expressed cell surface MAPA from binding to MAFA ligand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or a T-cell-expressed cell surface MAPA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition

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to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAPA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell for a cytotoxic tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is rat MAPA protein
                                                                                                                                                                                                                                                                                            CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mast cell function-associated antigen; MAFA, soluble; ligand, identification; screening, inflammation; inflammatory; allergy; allergic;
                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                          MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen (MAFA) -
useful for prevention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in combination with the MAFA to prevent inflammatory and allergic reactions
                                                                                                                                                                                                                                                                                                                                   LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ
                                                                                                                                                                                                            1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Partial sequence of mast cell function-associated antigen (MAFA)
                                                                                                                                                                                     ..
                                                                                                                                                     Length 188;
                                                                                                                                                                                 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel DNA encoding a mast cell function-associated useful for screening for ligands of MAFA which are
                                                                                                                                                    Score 838; DB 4;
Pred. No. 3.2e-82;
15; Mismatches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of inflammatory and allergic reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein; 114 AA.
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                                                                                                                                                     81.48;
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                                                                                                                                                                  80.78;
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                                                                                                                                                                  Best Local Similarity 80.7%
Matches 151; Conservative
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WICEKVL 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR77472 standard;
                                                                                                                        Sequence 188 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rattus rattus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     prevention.
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85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 NCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEEHTAW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents a novel human natural killer (NK) cell surface antigen, Kp43. This sequence can be used in a method resulting in the production of recombinant protein expressed by NK and T cells, which may inhibit cell-mediated cytotoxicity, e.g. in transplant rejection or autoimmune diseases, or may be used to produce antibodies for diagnostic or therapeutic use
                                                                                                                                                                                                                                                                                                                                        Kp43; human; natural killer cell surface antigen; NK; T cell; inhibitor; cell-mediated cytotoxicity; transplant rejection; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding natural killer cell surface antigen Kp43 - and transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14 GTLGIİCLSLMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCQEKWYGYRC
                                                                               CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK
                                                            121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILINSLIQRCGAIHRNGLQASSCEVALQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 RWEGGPALSLRILIN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cells for producing recombinant Kp43.
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                                                                                                                                                                                                                          AAW64791 standard; protein; 179 AA.
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(LOPE/) LOPEZ-BOTET M.
(BELT/) BELTRAN J A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lanier LL, Chang C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1998-530877/45.
                                                                                                                                                                                                                                                                                 (first
                                                                                                                        181 WICKKV 186
                                                                                                                                                                                                                                                                                                              Human Kp43 protein
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                                                                                                                                                    92 WVCKKV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic diseases, and tumour growth.
                                                                                              134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This is the amino acid sequence of human mast cell function- associated antigen (MAFA) splice variant huMAFA(E3/4-), which lacks the C-lectin-like domain of human MAFA (see AAMP8265) but retains the intracellular and transmembrane domains as well as the extracellular C-terminal tail. Truncated MAFA polypeptides including huMAFA(E3/4-), and polynucleotides encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-72), can be used be used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), or tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                              CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIG
                                                                                                                        1 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                  Gaps
                                                                                                                                                                        LRDIDGWRWEDGPALSLSILSNSVVOKCGTIHRCGLHASSCEVALQWICEKVL 113
                                                                                                                                                      LRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 68
                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 99;
                                                                                                                                                                                                                                                                                                                                                                           cell function-associated antigen; MAFA; huMAFA(E3/4-); ce variant; human; inflammation; allergy; asthma;
                                     Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            28; Indels
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Williams DH;
                                    Score 551; DB 2; L
Pred. No. 1.9e-51;
9; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 222.5; DB 2
Pred. No. 5.9e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13; Mismatches
                                                                                                                                                                                                                                                                                                                                               Human MAFA splice variant huMAFA(E3/4-).
                                                                                                                                                                                                                                                                                                                                                                                                        rheumatoid arthritis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lamont A,
                                                                                                                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 3; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PEPT-) PEPTIDE THERAPEUTICS LTD
                                                                                                                                                                                                                                                          standard; protein; 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.6%;
30.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98WO-GB001572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97GB-00011148
                                     53.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lamers MBAC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-059806/05.
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                                                     Local Similarity
Les 95; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAV84200
            Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 99 AA;
                                                                                                                                                                                                                                                                                                                   29-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9854209-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              03-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hewitt EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
                                                                                                                                                                                                                                                                                         AAW88267;
                                                                                                 75
                                                                                                                                                         135
                                                                                                                                                                                                                                                          AAW88267
                                                                                                                                                                                   61
                                       Query Match
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                                                         Best Loc
Matches
                                                                                                                                                                                                                               RESULT 6
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Gaps

70 84

129 LWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNY1CKQQL 178

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The type II integral membrane proteins (AAW40219-W40221) and CD94 (AAW40222) form a group which has 20% homology with the human macrophage antigen (TMAH) (AAW40215). The homology which TWAH shares with this group includes a series of disulphide residues. The structural homology between the peptides provides information on the structural and physical properties of both the TMAH gene and protein. This is used in the development of TWAH as a disapnostic tool and as a method of treating diseases associated with expression of TWAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71 NCYFISSEOKTWNESRHLCASOKSSLLOLONTDELDFMSS--SQOFYWIGLSYSEEHTAW 128
                                                                                                                                                                                                                                                                                                                                                                                       Human macrophage antigen - used for decreasing apoptosis associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTLGIICLSLMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCQEKWVGYRC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDSTCSHCPSCPILWTRNGS 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RWEGGPALSLRILTN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                     TMAH; apoptosis; osteoarthritis; diagnosis; treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 17.3%; Score 178.5; DB 2; Best Local Similarity 31.8%; Pred. No. 7.5e-11; Matches 54; Conservative 17; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 47; 58pp; English.
                                                                                                                                                                                                                                                                                                                                    Goli SK;
                           AAW40222 standard; peptide; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADE76965 standard; protein; 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLLTVILMSLLMYQRILCCGS
                                                                                                                                                                                                                                                  97WO-US013077.
                                                                                                                                                                                                                                                                              36006900-SD96
                                                                                   entry)
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                                                                                                                                                                                                                                                                                                      (INCY-) INCYTE PHARM INC
                                                                                                                                                                                                                                                                                                                                   Au-Young J,
                                                                                (first
                                                                                                                                                                                                                                                                                                                                                           WPI; 1998-130617/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                     osteoarthritis
                                                                                                                                                                Homo sapiens
                                                                                                                                                                                          WO9804585-A2
                                                                                                                                                                                                                                               22-JUL-1997;
                                                                                                                                                                                                                                                                            31-JUL-1996;
                                                                                                                                                                                                                                                                                                                               Hillman JL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29-JAN-2004
                                                                               07-JUL-1998
                                                                                                                                                                                                                      05-FEB-1998.
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                                                     AAW40222
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                                                                                                          CD94.
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ID ADE7
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AC ADE7
XX
DT 29-5
RESULT 8
              AAW40222
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The invention relates to a composition comprising several cDNAs that are differentially expressed in a liver disorder. The composition is useful for treating liver disorder such as hyperlipidaemia, hypertension, type II diabetes, tumours of the liver and disorders of the inflammatory and immune response. The composition is useful for a high-throughput method of screening several molecules or compounds to identify a ligand which specifically binds a cDNA. A protein encoded by the cDNA is useful for a high-throughput method for using a protein to screen several molecules or compounds to identify at least one ligand which specifically binds the protein encoded by the cDNA with several of molecules or compounds under conditions to allow specific linding, and detecting specific binding between the protein and a molecule or compound, therefore identifying a ligand which specifically binds the protein. The composition is useful for detecting and conditions to allow differential gene expression, can be used in gene therapy, to formulate prognosis and to design a treatment regimen and to monitor the efficacy of treatment. The present sequence represents the amino acid is sequence of a protein encoded by a cDNA differentially expressed in a
                                                                                                                                                                                                                                                                                                                                                                                                                                     Composition comprising several cDNAs that are differentially expressed in treated human C3A liver cell cultures, useful for treating liver
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71 NCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEEHTAW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               70
                               human; liver disorder; hyperlipidaemia; hypertension; type II diabetes; tumour; liver; inflammatory disorder; immune response disorder; high-throughput screening; differential gene expression; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               85 HCYYFSMEXKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 RWEGGPALSLRILTN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17.3%; Score 178.5; DB 8;
31.8%; Pred. No. 7.5e-11;
ive 17; Mismatches 68;
Human protein expressed in a liver disorder #36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 130; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM80296 standard; protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44 GLLTVILMSLLMYQRILCCGS
                                                                                                                                                                                                                         30-JUL-2001; 2001US-00919039.
                                                                                                                                                                                                                                                               28-JUL-2000; 2000US-0222113P.
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Best Local Similarity 31.8%
                                                                                                                                                                                                                                                                                                                                                                                WPI; 2004-031227/03.
                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; ADE76964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 179 AA;
                                                                                                                                                  JS2003108871-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     liver disorder
                                                                                                                                                                                                                                                                                                       (KASE/) KASER
                                                                                                                                                                                        12-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               disorders
                                                                                                                                                                                                                                                                                                                                            Kaser MR;
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AAM80296
ID AAM80
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AC AAM80
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Gaps

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The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynuclaotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, immunoomodulatory activity and activity, rissue growth factor activity, immunoomodulatory activity and activity, or activity, immunoomodulatory activity and activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70 SHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQCVKLFGEYLGQD 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 FYWIGL-RNIDGWRWEGGPALSLRIL----TNSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                             cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21 ARCQQCPPGWVLSBEHCYYFSAEAQAWEASQAFCSAYHATLDFLLSHTQ--DFLGRYPVSR
                                                                                                            vaccine, peptide therapy; stem cell growth factor; haematopolesis;
tissue growth factor; immunomodulatory; cancer; leukaemia;
nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match 16.3%; Score 167.5; DB 4; Length 142; Local Similarity 30.6%; Pred. No. 8.6e-10; Los 37; Conservative 15; Mismatches 62; Indels 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drmanac RT, Asundi V, Zhou P, Xi
Wang D, Wang J, Zhang J, Ren F,
Wejhrman T, Goodrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 20; Page 6210-6211; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                              01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-0065551.
20-OCT-2000; 2000US-00653325.
30-NOV-2000; 2000US-00728422.
                                                                                                                                                                                                                                                                                                                                                 03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-UUX-2000; 2000US-00590075.
19-UUL-2000; 2000US-00620325.
                                                       Human protein SEQ ID NO 3948.
                                                                                                                                                                                                                                                                                                                05-FEB-2001; 2001WO-US004098.
                  06-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tang YT, Liu C,
Ma Y, Zhao QA, 1
Xue AJ, Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAK53429.
                                                                                           cytokine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 142 AA;
                                                                                                                                                                                                                                  WO200157190-A2.
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                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                         09-AUG-2001
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Matches
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Xu C, Cao Y; Chen R, Wang ZW;

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The invention relates to an isolated polymucleotide encoding a cytokine or cell proliferation/differentiation-related protein (or the mature protein or active domain, sequences greater than 9% identical to it or sequences complementary to it. Also included are the encoded proteins, expression vectors, transformed host cells, antibodies, and identifying a compound that binds to the polymptide They are particularly useful therapeutic, diagnostic or research methods. They are particularly useful therapeutic, diagnostic or research methods. They are particularly useful thrombocytopaenia, osteoporosis, osteoarthritis, inflammations, ulcers, alzheimer's disease, Parkinson's disease, Huntington's disease, thrombocytopaenia, osteoporosis, osteoarthritis, inflammations, amount of a myotrophic lateral sclerosis, stroke, immune deficiencies (e.g. human immunodeficiency virus (HTV), severe combined immunodeficiency or infections), autoimmune disorders (e.g. rheumatoid arthritis, Guillain-Barre syndrome or graft-versus-host disease), cancers (e.g. thyroid cancer, lung cancers, small cell carcinoma, Kaposi's sarcoma, brain tumours, prostate cancer, ovarian cancer or leukaemias), or inflammatory disorders (e.g. rheum cancer or leukaemias), or inflammatory disorders (e.g. rheumacor). The
                                                                                                                                                                                                          wound; ulcer; thrombocytopaenia; osteoporosis; osteoarthritis; inflammation; Alzheimer's disease; Parkinson's disease; stroke; thuntington's disease; amyotrophic lateral sclerosis; HIV; immune deficiency; human immunodeficiency virus infection; evere combined immunodeficiency; infection; autoimmune disorder; rheumatoid arthritis; Guillain-Barre syndrome; graft-versus-host disease; cancer; thyroid cancer; lung cancer; syndrome; graft-versus-host disease; kaposi's sarcoma; brain tumour; prostate cancer; ovarian cancer; leukaemia; inflammatory disorder; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides for diagnosing, treating or preventing e.g. anemia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Yang
                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; anaemia;
                                                                                                                                                     Human cytokine or cell proliferation/differentiation protein #6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inflammations,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Wehrman T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  wounds, ulcers, thrombocytopenia, osteoporosis, inflammations
Alzheimer's disease, stroke, autoimmune disorders or cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asundi V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Liu C,
                                    ABG72616 standard; protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 19; Page 60; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                        Crohn's disease; food supplement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goodrich R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-JAN-2001; 2001US-00774434.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
                                                                                                                (first entry)
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DRMANAC R T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZHOU P.
GOODRICH R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEHRMAN T.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LIU C.
ASUNDI V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TANG Y T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; ABX13629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US2002137044-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                  12-FEB-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-SEP-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drmanac RT;
                                                                           ABG72616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ΥΤ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WEHR/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TANG/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (GOOD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (ASUN/)
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RESULT 11
                    ABG72616
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3,
                                                                                                                                                                  70 SHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQD 129
                                                                                                                                                                                                                       130 FYWIGL-RNIDGWRWEGGPALSLRIL----TNSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                   HSWVGAWRGPQGWHWIDEAPLPPQLLPEDGEDNLDINCGALEEGTLVAANCSTPRPWVCA 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                                                                                        21 ARCQOCPPGWVLSEEHCYYFSAEAQAWEASQAFCSAYHATLPLLSHTO--DFLGRYPVSR 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, cytokine, cell proliferation, cell differentiation, gene therapy, vaccine, peptide therapy, stem cell growth factor, haematopolesis, tissue growth factor, immunomodulatory, cancer, leukaemia, nervous system disorder, arthritis, inflammation.
polynucleotides and proteins are useful for screening peptides or small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cao Y;
R, Wang ZW;
           molecule inhibitors or agonists that are useful for treating these diseases. The polypeptide is also useful as molecular markers, or as food supplement. The present sequence is a cytokine or cell proliferation/differentiation-related protein of the invention
                                                                                                                                           Gaps
                                                                                                                                           7;
                                                                                                               DB 6; Length 142;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asundi V, Zhou P, Xu C,
J, Zhang J, Ren F, Chen
Goodrich R;
                                                                                                                                         Indels
                                                                                                                                         62;
                                                                                                           16.3%; Score 167.5; DB 6 30.6%; Pred. No. 8.6e-10; ive 15; Mismatches 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 20; Page 477; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                           AAM80302 standard; protein; 160 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drmanac RT, P
Wang D, Wang C
Wejhrman T, G
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human protein SEQ ID NO 3960.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
20-JUN-2000; 2000US-00598075.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000US-00620325.
2000US-00654936.
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2000US-00693325.
2000US-00728422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                        37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
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                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tang YT, Liu C,
Ma Y, Zhao QA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-476283/
N-PSDB; AAK53435
                                                                                  Sequence 142 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200157190-A2
                                                                                                                                                                                                                                                                               K 185
                                                                                                                                                                                                                                                                                                       K 139
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20-JUN-2000;
19-JUL-2000;
01-SEP-2000;
15-SEP-2000;
20-OCT-2000;
30-NOV-2000;
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                                                                                                                                                                                                                                                                               185
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                                                                                                                                      Matches
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           production of other cytokines in other cell populations. The polymucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy, The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                            70 SHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQD 129
                                                                                                                                                                                                                                                                                                                 130 FYWIGL-RNIDGWRWEGGPALSIRIL----TNSLIQRCGAIHRNGLQASSCEVALQWICK 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Secreted protein, anti-inflammatory; immune stimulant; suppressant; human; cytokine; autoimmune disease; regulator; activin; inhibin; G52-24.
                                                                                                                                                                                                                                                                        96
 or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acids encoding novel secreted proteins - useful e.g. as an anti-inflammatory, immune stimulant or suppressor, etc.
                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                   7;
                                                                                                                                                                                           Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "predicted mature amino acid sequence"
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                                                                                                                                                                                                                    Indels
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cell proliferation or cell differentiation
                                                                                                                                                                                                                    62;
                                                                                                                                                                                        DB 4;
                                                                                                                                                                                        16.3%; Score 167.5; DB 30.6%; Pred. No. 1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Racie LA, Lavallie ER,
                                                                                                                                                                                                                 15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                AAW27288 standard; protein; 181 AA.
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/label= signal
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/label= G52-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human G52-24 secreted protein.
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97US-00781226
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                                                                                                                                                                                                                 37; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-535835/49.
                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAT91295.
                                                                                                                                                               Sequence 160 AA;
                                                                                                                                                                                                                                                                                                                                                     K 185
                                                                                                                                                                                                                                                                                                                                                                               K 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-APR-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-JAN-1997;
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                                                                                                                                                                                                                                                                     39
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42;
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                                                                                                                             02-JUN-1997
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                                                                                                                                                                                                                                                                             Merberg D,
Kelleher K;
                                                                                                                                                                                                                                                             Jacobs K,
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                                    This sequence represents a novel secreted protein, G52-24, isolated from a clone, G52-24 (ATCC 98028), derived from a human PBMC cDNA library. The nucleic acid and encoded G52-24 secreted protein can be used for research purposes (as markers for tissues, molecular weight markers for gels, primers, probes, etc.), for nutrition (as C, N or carbohydrate source), as a cytokine for cell proliferation and differentiation activity, as immune stimulatts or suppressors e.g. for viral, bacterial or fungal infections, for autoimmune diseases such as multiple sclerosis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNIDG--WRWEGG-----PA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSORFCDSODADLAQVESFOELNFLLRYKGPSDHWIGLSREQGOPWKWINGTEWTROFFI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                             97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LFFLIMFLTIIVCGMVAALSAIRANCHQEPSVCLQAACPESWIGFQRKCFYFSDDTKNWT 87
                                                                                                                                                                                                                  systemic lupus erythematosus, to regulate haematopoiesis, for tissue growth, as an activin or inhibin, or having chemotactic, chemokinetic, haemostatic and thrombolytic, receptor/ligand, anti-inflammatory or
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMSLLMYQRILCCG-----SKDSTCSHCPS-----CPILWTRNGSHCYYFSMEKKDWN
                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                 29;
                                                                                                                                                                                                                                                                                                                                                                          Length 181;
                                                                                                                                                                                                                                                                                                                                                                                                               67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       immune disorder; severe combined immunodeficiency; SCID;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----AGECAYLNDKGASSARHYTERKWICSK 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LSLRILINSLIQRCGAIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                          DB 2;
                                                                                                                                                                                                                                                                                                                                                                      Score 160.5; DB 2
Pred, No. 6.8e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                 19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADC38664 standard; protein; 181 AA
Claim 8; Page 59; 81pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-00628364.
96US-00635311.
96US-00659224.
96US-00664596.
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96US-00686878.
96US-00701819.
96US-00721488.
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                                                                                                                                                                                                                                                                                 tumour inhibitory activities
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                               Sequence 181 AA;
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27-SEP-1996;
27-SEP-1996;
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26-JUL-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                 42;
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The invention relates to a protein comprising fully defined AZ302 I

C protein or BD127 1 6 protein. The polynucleotides are useful for

C expressing recombinant proteins for analysis and are also useful as

C chromosome markers or tags to identify chromosomes or to map related gene

C chromosome markers or tags to identify chromosomes or to map related gene

CC constitues. The proteins are useful as amino acid supplement, carbon

Source, nitrogen source and carbohydrate source. The proteins are useful

CC combined immunodeficiency (SCID); autoimmune disorders (e.g. severe

CC combined immunodeficiency (SCID); autoimmune disorders (e.g. multiple

CC reactions (e.g. asthma), myeloid or lymphoid cell deficiencies,

CC reactions (e.g. asthma), myeloid or lymphoid cell deficiencies,

CC reactions (e.g. asthma), myeloid or lymphoid cell deficiencies,

CC osteoporosis or osteoarthritis, peripheral nervous system disease),

CC peripheral neuropathy, Alzheimer's disease, Parkinson's disease),

CC coagulation disorders; inflammatory diseases (e.g. systemic inflammatory

CC reponse syndrome (SIRS), ischaemia-reperfusion injury, Crobn's disease),

CC canpulation immunity, for inducing bone, cartilage, tendon, ligament and/or

CC repenrating nerve and brain tissue, for inducing fertility and for

CC inhibiting tumour growth. Proteins are also useful as othendrine for

CC inhibiting tumour growth. Proteins are also useful as achemokine for

CC inhibiting tumour growth. Proteins are also useful as achemokine for

CC inhibiting tumour growth. Proteins are also useful as achemokine for

CC inhibiting tumour growth. Proteins are also useful as achemokine for

CC inhibiting tumour growth for present and also

CC inhibiting tumour growth for present and also

CC sequence represents the amino acid sequence of a human secreted protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Proteins A23021 encoded by clone A23021 from human adult colon, and BD12716 encoded by clone BD12716 from human fetal kidney cDNA library, useful for treating e.g. multiple sclerosis and rheumatoid arthritis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Σ,
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Spaulding V, Carlin-Duckett
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67;
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26.8%; Pred. No. 6.8e-09;
iive 19; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  50 LMSLLMYQRILCCG----SKDSTCSHCPS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 22; 412pp; English.
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                                                                             96US-00739775.
96US-00721926.
96US-00738367.
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N-PSDB; ADC38663.
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08-NOV-2000;
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    Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV; cardiant; vascular; cardiant; vascular; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzheimers; immunodeficit; opticis, multiple solerosis; candianzheimers; immunodeficiency virus; rheumatoid arthritis; multiple solerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma; Sezary syndrome; Gaucher's disease; neurological disease; baltainer; disorder; cardiac arrest; tachycardia; andina; infection; corneal infections; wound healing; immunogen; gene therapy; antisense; food additive.
                            extracellular matrix protein, Seq ID No 310
                                                                                                                                                                                                                                                                                                                          2000US-0179065P.
2000US-018664P.
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2000US-0189874P.
2000US-0199076P.
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2000US-0229343P.
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(first entry)
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                                                                                                                                                                                                               Homo sapiens
04-DEC-2001
                            Human novel
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The invention relates to isolated nucleic acid molecules encoding novel.

human secreted extracellular matrix proteins (SPS). The polymucleotides
and proteins are used to prevent, treat a medical condition in e.g.

thumans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For
example, disorders associated with decreased expression of SPS. The SP
polymucleotide or a vector expressing them may be administered to treat
diseases by gene therapy. Antisense molecules may be administered to down
regulate expression of SPS by binding with the cells own genes and
probes in diagnostic assays. The SPS may also be used as DNA
probes in diagnostic assays. The SPS may also be used as DNA
probes in diagnostic assays. The SPS may also be used to
produce antibodies and to identify modulators (agonists and antagonists)
of the SPS. The anti-(SP) antibodies and antagonists and she antipodies and activity of SP and as diagnostic agents for
down regulate expression and activity of SP and as disorates include for
cample immune/autonimmune diseases (e.g. HIV (human immunodeficiency
virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis),
cancers and hyperproliferative disorders (e.g. melanomas, neoplasms of
the breast or liver, Sezary syndrome and Gaucher's disease), neurological
diseases (e.g. Alzheimer's disease, Parkinson's disease), neurological
concers and subscretus (e.g. cardiac arrest, tachycardia and andisorders
concers and bycertions, viruses and fungi and ocular disorders
concers and bycertions. Other uses include wound healing, maintenance
cof organs before transplantation, support of cell culture of primary
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
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N-PSDB; AAS31231.
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Matches 40; Conserv
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Search completed: August 10, 2004, 16:42:20 Job time : 48.5 secs

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August 10, 2004, 16:44:06; Search time 39.5 Seconds (without alignments) 1492.972 Million cell updates/sec
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1 MADSSIXSTLELFEAPQVQD.......GLQASSCEVALQWICKKVLY 188
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/USO6_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/USO8_NEW_PUB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9F_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/USO9F_NEW_PUB.pep:*
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13: /cgn2_6/ptodata/2/pubpaa/USO9F_PUBCOMB.pep:*
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16: /cgn2_6/ptodata/2/pubpaa/USO9F_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/2/pubpaa/USO0_PUBCOMB.pep:*
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1291235 seqs, 313682936 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                  - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Minimum DB seq length: 0
Maximum DB seq length: 188
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Sequence 3, Appli	Sequence 130, App	Seguence 10. Appl	Sequence 22, Appl	Sequence 310, App	Segmence 310, App	Sequence 98, Appl	Sequence 98, Appl	Sequence 4, Appli	Sequence 466. App	Sequence 466, App	Semience 340. App	Sequence 486. App	Sequence 340, App
SUMMARIES	US-09-811-367B-3 US-09-811-367B-5	US-09-919-039-130	US-10-335-009-10	US-10-114-893-22	US-09-764-870-310	US-10-125-540-310	US-09-759-130B-98	US-10-741-790-98	US-10-335-009-4	US-09-764-870-466	US-10-125-540-466	US-09-764-870-340	US-09-764-870-486	US-10-125-540-340
DB	 00	10	15	13	σ	14	10	16	15	σ	14	6	σ	14
% Query Match Length DB	188	179	179	181	182	182	165	165	132	94	94	140	140	140
% Query Match	100.0	17.3	17.3	15.6	15.2	15.2	15.0	15.0	14.7	14.4	14.4	14.4	14.4	14.4
Score	1029	178.5	178.5	160.5	156	156	154	154	151	148.5	148.5	148.5	148.5	148.5
Result No.	42	3	4	Ŋ	9	7	œ	σ	10	11	12	13	14	15

Semience 486	Sequence 33902. A	Sequence 108, App	Sequence 108, App	Sequence 1275, Ap	Sequence 5855, Ap	Sequence 11, Appl	Sequence 32, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 83, Appl	Sequence 83, Appl	Sequence 6, Appli	Sequence 55, Appl	Sequence 2, Appli	Sequence 100, App	Sequence 100, App	Sequence 85, Appl	Sequence 85, Appl	Sequence 86, Appl	Sequence 86, Appl	12,	3,	Sequence 2, Appli	Sequence 90, Appl	67,	Sequence 836, App	Sequence 11, Appl	Sequence 11, Appl	Sequence 6, Appli
14 IIS-10-125-540-486	9 US-09-864-761-33902	10 US-09-759-130B-108	16 US-10-741-790-108	12 US-10-296-115-1275	14 US-10-106-698-5855	10 US-09-284-320-11	13 US-10-114-893-32	14 US-10-088-859-2	14 US-10-179-528-1	10 US-09-759-130B-83	16 US-10-741-790-83	9 US-09-944-807-6	10 US-09-766-511B-55	14 US-10-270-470-2	LO US-09-759-130B-100	L6 US-10-741-790-100	LO US-09-759-130B-85	L6 US-10-741-790-85	L0 US-09-759-130B-86	16 US-10-741-790-86	16 US-10-775-640-12	12 US-10-239-656-3	L2 US-10-239-656-2	L2 US-10-239-656-90	L2 US-09-964-956-67	L2 US-10-072-012-836	9 US-09-929-230-11	14 US-10-226-420-11	L5 US-10-335-009-6
140	35	145	145	146	137	149	149	149	149	188	188	149	161	162	138	138 1	162	162	187	187	187	133	143	162	124	124	158	158	149
14.4	14.3	14.1	14.1	14.1	14.0	14.0	14.0	14.0	14.0	13.9	13.9	13.9	13.8	13.8	13.6	13.6	13.6	13.6	13.3	13.3	13.3	13.1	13.1	13.1	12.6	12.6	12.6	12.6	12.5
148.5	147	145	145	145	144	144	144	144	144	143.5	143.5	143	142	142	140	140	140	140	137	137	137	135	135	135	129.5	129.5	129.5	129.5	129
16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Patent No. US20020155110A1

Patent No. US20020155110A1

Patent No. US20020155110A1

APPLICANT: GENINI SCIENCE, INC.

APPLICANT: GENINI SCIENCE, INC.

APPLICANT: Takahashi, No. US20020155110Aluaki

APPLICANT: Takahashi, No. US20020155110Aluaki

APPLICANT: Mikayama, Toshifumi

TITLE OF INVENTION: PHARMACHUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THE FILE REFERENCE: 021286/0278719

TITLE OF INVENTION: UNDER: US/09/811,367B

CURRENT FAPLICATION NUMBER: 60/190,716

PRIOR APPLICATION NUMBER: 60/190,716

PRIOR FILING DATE: 2000-03-17

NUMBER OF SEQ ID NOS: 20

SOFTWARE: PATENTIN VERSION 3.0

SEQ ID NO 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
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Best Local Similarity 100.
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Mus musculus
US-09-811-367B-3
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7;

Gaps

31;

-- KDSTCSHCPSCPILWTRNGS

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85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
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                                                                                                                                                                                                                                                      85 HCYYFSMEKKDWNSSLKFCADKGSHLLIFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                                                                                                                                                                  71 NCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEEHTAW 128
                                                                                                                                                                                  14 GILGIİCLSLMATLGİLLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCQEKWVGYRC 70
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APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Bowman, Michal R.
APPLICANT: Spaulding, Vikki
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14 GTLGIICLSLMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCQEKWVGYRC
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                                                                                                                                                                                                                                                                                                                                                                                         142 RWEGGPALSLRILTN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10, Application US/10335009
Publication No. US20040001804A1
GENERAL INFORMATION:
APPLICANT: POTUNEINON:
APPLICANT: POTUNEINON:
TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION
FILE REFERENCE: 11707.02/469887-7
CURRENT APPLICATION NUMBER: US/10/335,009
CURRENT FILING DATE: 2002-12-31
FRIOR APPLICATION NUMBER: US 09/475,365
FRIOR FILING DATE: 10999-12-30
NUMBER OF SEQ ID NOS: 11
DB 10; Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    129 LWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL
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                                                            68; Indels
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Pred. No. 1.3e-10;
                                 Pred. No. 1.3e-10;
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31.8%; Pred. No. ...
17; Mismatches
                                                            17; Mismatches
   17.3%; Score 178.5;
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                                                                                                                                44 GLLTVILMSLLMYQRILCCGS---
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APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa A.
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GENERAL INFORMATION:
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                                 31.8%;
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Best Local Similarity 31.89
Matches 54; Conservative
                                                                   54; Conservative
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                                     Similarity
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US-10-114-893-22
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US-10-335-009-10
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   Query Match
Best Local S
Matches 54
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APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Mikayama, Toshifumi
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM
FILE REFERENCE: 021286/0278719
CURRENT APPLICATION UNMERE: US/09/811,367B
PRIOR APPLICATION NUMBER: 60/190,716
PRIOR APPLICATION NUMBER: 60/190,716
PRIOR FILING DATE: 2000-03-17
WINNERSON OF GENERAL OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE WASTON OF THE W
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APPLICANT: Kaser, Matthew R.

TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: 60/222,113

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL Program

SEQ ID NO 130
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; OTHER INFORMATION: Incyte ID No. US20030108871A1 516300CD1
US-09-919-039-130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21; Indels
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; Pred. No. 1.4e-80;
15; Mismatches 21;
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Publication No. US20030108871A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                      Sequence 5, Application US/09811367B Patent No. US20020155110A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.0
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80.7%;
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Best Local Similarity 80.7%
Matches 151; Conservative
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                                           WICKKVLY 188
                                                                                                        181 WICKKVLY 188
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US-09-919-039-130
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31; Gaps

Length 179;

70 84

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NUMBER OF SEQ ID NOS: 460
                  FILE REFERENCE: PTZ14C1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28 LFFLIMFLTIIVCGMVAALSAIRANCHQEPSVCLQAACPESWIGFQRKCFYFSDDTKNWT 87
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CURRENT APPLICATION NUMBER: US/09/764,870

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ 1D NOS: 646

SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15.2%; Score 156; DB 9; Length 182; 29.2%; Pred. No. 3.1e-08;
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Publication No. US20030059875A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
ITILE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 310, Application US/09764870; Patent No. US20020042386A1; GENERAL INFORMATION:
; APPLICANT: Rosen et al.; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
                                                                                                                                                                                                                                                                                                              67; Indels
                                                                                                                                                                                                                                                                      ch 15.6%; Score 160.5; DB 13; Similarity 26.8%; Pred. No. 1e-08; 42; Conservative 19; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 LSLRILTNSLIQRCGAIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | :: || | | LG-----AGECAYLNDKGASSARHYTERKWICSK 176
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FILE REFERENCE: GI 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT FILING DATE: 2002-04-02
FARLIER APPLICATION NUMBER: 09/413,232
FARLIER FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SEQ ID NO 22
LENGTH: 181
                                                                                                                                                                                                                                                                                                                                                   ----SKDSTCSHCPS-
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                                                                                                                                                                                      TYPE: PRT
CRGANISM: Homo sapiens
US-10-114-893-22
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Best Local Similarity
Matches 42; Conserva
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US-10-125-540-310
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US-09-764-870-310
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LENGTH: 182
TYPE: PRT
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APPLICANT: MCCATCHY, Sean A
APPLICANT: Braser, Christopher C
APPLICANT: Branes, Thomas S
APPLICANT: Branes, Thomas S
APPLICANT: Markay, Charles R
APPLICANT: Kirst, Susan J
APPLICANT: Kirst, Susan J
APPLICANT: Werst, Paul S
APPLICANT: Weighten, Nicolas
APPLICANT: Weighten, Nicolas
APPLICANT: Weighten, Nicolas
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: PROGNOSTIC, PREVENTIVE, THERAPBUTIC, AND OTHER
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES:
TITLE OF INVENTION NUMBER: US/09/759,130B
CURRENT FILING DATE: 2002-09-16
                                                                                                                                                                                                                                                                                                                                                                                                                           60 LCCG-SKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                             53 LCASRSADQTV----LCQSEWLKYQGKCYWFSNEMKSWSDSYVYCLERKSHILIHDQLE 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  119 VKLFGEYLGQ-DFYWIGLRNID---GWRWEGGPALSLRIL------TNSLIQRCGAIHR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20;
                                                                                                                                                                                                                                                                                                                   Length 182;
                                                                                                                                                                                                                                                                                                                                                                       Indels
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 310
LENGTH: 182
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PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR PELING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR PILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
PRIOR PRILING DATE: 2000-06-29
PRIOR PILING DATE: 1999-06-29
PRIOR PILING DATE: 1999-06-10
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR PILING DATE: 1999-09-10
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Publication No. US20030022279A1
GENERAL INFORMATION:
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                                                                                                                                                                                                TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 40; Conserv
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US-09-759-130B-98
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US-10-741-790-98
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APPLICANT: Kiret, Susan J
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Goodearl, Andrew
APPLICANT: Goodearl, Andrew
APPLICANT: Marieman, Douglass BENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
CURRENT APPLICATION NUMBER: US 99/49, 49
PRICR PLING DATE: 2000-01-07
PRICR PLING DATE: 2000-04-27
PRICR PLING DATE: 2000-04-27
PRICR PLING DATE: 2000-04-27
PRICR PLING DATE: 2000-05-30
PRICR PLING DATE: 2000-05-30
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PRICR PLING DATE: 2000-06-30
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                                                                                                                                                                                                                                                                                                                                            40 MVALGLLTVIL----MSL-LMYQRILCCGSKD---STCSHCPSCPILWTRNGSHCYYFSM 91
                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                               Indels 18;
                                                                                                                                                                                                                     15.0%; Score 154; DB 10; Length 165; 28.6%; Pred. No. 4.5e-08; tive 26; Mismatches 71; Indels 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 LSLRILTNSLIQRCGAIHRNGL----QASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals,
APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 98, Application US/10741790 Publication No. US20040121396A1
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Kirst, Susan J
Mackay, Charles R
Myers, Paul S
Leiby, Kevin R
                                                                                                                                                                                                                        Query Match 15.0%
Best Local Similarity 28.6%
Matches 46; Conservative
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ORGANISM: Homo sapiens
                                                                                                                          ; ORGANISM: Homo sapiens
US-09-759-130B-98
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US-10-741-790-98
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                                   SEQ ID NO 98
LENGTH: 165
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APPLICANT:
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                                                                                                                                                                                                              92 EKKDWNSSLKFCADKGSHLLIFPDNQGVKLFGEYLGQDFYWIGL---RNIDGWRWEGGPA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62 CGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKL 121
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                                                                                                                                               8; Gaps
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TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION
FILE REPERENCE: 11707.02/469647-70
CURRENT APPLICATION NUMBER: US/10/335,009
CURRENT FILING DATE: 2002-12-31
PRICR APPLICATION NUMBER: US 09/475,365
PRICR FILING DATE: 199-12-30
NUMBER OF SEQ ID NOS: 11
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Sequence 466, Application US/09764870
Batent No. US20020042386A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PT214
CURRENT RELIAG DATE: 2.001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: PatentIn Ver. 2.0
                         Length 165;
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                                                                      71; Indels
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28.9%; Pred. No. 7.1e-08;
                    15.0%; Score 154; DB 16; 28.6%; Pred. No. 4.5e-08; iive 26; Mismatches 71;
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US-10-335-009-4
; Sequence 4, Application US/10335009
; Publication No. US2004001804A1
; APPLICANT: Porunelloor , Mathew A.
; APPLICANT: Porunelloor , Mathew A.
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Matches 37; Conservative
                                                                      Conservative
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Query Match
Best Local Similarity
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LENGTH: 94
TYPE: PRT
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ORGANISM: Homo sapiens
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Matches 32; Conserv
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                                                                                                                 ; ORGANISM: HOMO
US-09-764-870-340
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US-09-764-870-486
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                              NAME/KEY: SITE
LOCATION: (52)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
                                                                                                    ; LOCATION: (68); ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-764-870-466
                                                                                                                                                                                                                                        70 SHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQD 129
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... OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino US-10-125-540-466
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PTZ14
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
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Publication No. US20030059875A1
GENERAL INFORMATION:
TILE OF INVENTION:
TILE REFERENCE: P7214C1
CURRENT APPLICATION UNDBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
NUMBER OF SEQ ID NOS: 646
SOFTWARE PatentIn Ver. 2.0
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                                                                                                                                                                       ch 14.4%; Score 148.5; DB 9;
1 Similarity 36.2%; Pred. No. 8.7e-08;
29; Conservative 10; Mismatches 38;
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36.2%; Pred. No. 8.7e-08;
tive 10; Mismatches 38;
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Patent No. US20020042386A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 29, Conserva
                                                                                  NAME/KEY: SITE
LOCATION: (68)
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US-09-764-870-340
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Best Local S:
Matches 29
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69 CSHCPS-CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHILITFPDNQGVKLFGEYLG 127
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         wrapper
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT214
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                     Indels
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Prior application data removed - consult PALM or file
NUMBER OF SEQ ID NOS: 646
SOFWARR: PatentIn Ver. 2.0
SEQ ID NO 340
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TITLE OF INVENTION: Nucleic Acids, Proteins, and AntiFILE REFERENCE: PT214C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Frior Application removed - See File Wrapper or Palm
                                                                                                                                                                                                                                                                64;
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                                                                                                                                                                                                                 14.4%; Score 148.5; DB 9 26.2%; Pred. No. 1.4e-07; ive 23; Mismatches 64
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Best Local Similarity 26.2%
Matches 32; Conservative
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                                                                                                                  TYPE: PRT
ORGANISM: Homo sapiens
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69 CSHCPS-CPIIMTRNGSHCYYFSMEXKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLG 127
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                                                                                                                                                                                                                                                            3; Gaps
                                                                                                                    Query Match
Best Local Similarity 26.2%; Pred. No. 1.4e-07;
Matches 32; Conservative 23; Mismatches 64; Indels 3;
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; NUMBER OF SEQ ID NOS: 646
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 340
; LENGTH: 140
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-125-540-340
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us-09-811-367b-3.closed.rai

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INFORMATION FOR SEQ 1D NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
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Best Local Similarity
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5: /cgn2_6/ptcdata/2/iaa/6B_COMB.pep:*
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US-08-69-342-3
US-08-650-578-2
US-08-68-342-3
US-09-113-788-3
US-09-113-789-9
US-08-722-126A-9
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US-08-543-246B-19
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
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GenCore version
Copyright (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Minimum Match 0%
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Listing first 45 summaries
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Sequence 21, Appl Sequence 15, Appl Sequence 18, Appl Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 4, Appli Sequence 4, Appli Sequence 326, Appli Sequence 326, Appli Sequence 6, Appli Sequence 6, Appli Sequence 17, Appl Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli	A MAST CELL GEN (MAFA)
US-09-531-056A-21 US-09-531-056A-16 US-09-531-056A-18 US-07-614-433A-2 US-07-614-433A-2 US-07-893-929A-4 US-07-893-929A-4 PCT-US92-10344-4 US-09-489-847-365 US-09-489-847-366 US-09-489-847-366 US-09-489-847-366 US-09-893-929A-6 US-07-893-929A-6 US-08-92-10344-6 US-08-92-10344-6 US-08-92-10344-6 US-08-92-10344-6 US-08-92-10344-6 US-08-92-10344-6 US-08-92-10344-6 US-08-92-10344-6 US-08-92-10344-6 US-08-92-10344-6 US-08-92-10344-6 US-08-92-10344-6 US-08-92-10344-6 US-08-92-10344-6	IGNMENTS IGNMENTS OCIATED ANTI P.L.L.C, Ste. 300 ICA S, Version # 126A
44444111122211222212222222222222222222	on Is Is Is SH SH SH SH SH SH SH SH SH SH SH SH SH
	SULT 1 Sequence 5, Application US/08 Patent No. 604427 GENERAL INFORMATION APPLICANT: GUTHMANN, MARC APPLICANT: GUTHMANN, MARC APPLICANT: TALL, MICHAEL TITLE OF INVENTION: FUNCT MUBER OF SEQUENCES: 20 CORRESPONDENCES ADDRESS: ADDRESSEE: ROWDY AND N STREET: 1419 Seventh Str CITY: Washington STRATE: D.C. COUNTY: Washington STATE: D.C. COUNTY: WASHINGTON STATE: D.C. COUNTY: WASHINGTON STATE: D.C. COUNTYER READABLE FORM: MEDIUM TYPE: FIDAPY dis COMPUTER: DEPLICATION SOFTWARE: PATENTION DATA: APPLICATION NUMBER: US/ FILING DATE: 08-CT-199 CLASSIFICATION NUMBER: US/ FILING DATE: 06-APR-199 RIGHS APPLICATION NUMBER: IL FILING DATE: 06-APR-199 REPERENCE/DOCKET NUMBER: IL FILING DATE: 08-APR-199 ATTORNEY/AGENT INFORMATION NAME: BROWDY, ROGE I. REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION NAME: BROWDY, ROGE I. REFERENCE/DOCKET NUMBER: TELEGOMMUNICATION INFORMATION TELEFAX: (202) 737-3528
127 127 127 124.5 124.5 124.5 124.5 120 110 111 111.5 114.5	SEQUENCE 5. APPLICAT Detent No. 6034227 GENERAL INCOMMATION APPLICANT: GUTHM APPLICANT: GUTHM APPLICANT: GUTHM APPLICANT: TAL, TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION TITLE OF INVENTION STATE: 419 Sec CITY: Washingt. STATE: 419 Sec CITY: Washingt. STATE: D.C. COUNTRY: UNITE ZIP: 20004 ATE ZIP: 20004 ATE COMPUTER READABLE MEDIUM TYPE: F MEDIUM TYPE: F MEDIUM TYPE: PATE ZIP: 20004 ATE ZIP: 20004 ATE SPELICATION NUM FILING DATE: 00 FILING
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Length 188;

Score 838; DB 3; Pred. No. 1.8e-86;

81.4%; 80.7%;

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75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIG 134
121 LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180
                          1 CPNI,WMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG
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                                                                                                                                                                                                                                                                                                APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: Patentin Release #1.0, Version #1.30
SOCTWARE: Patentin Release #1.0, Version #1.30
SOCTWARE: PATENTIN BATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 06-APR-1996
PRIOR APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION NUMBER: IL 109257
FILING DATE: 06-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53.5%; Score 551; DB 3;
84.1%; Pred. No. 2e-54;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: UNITED STATES OF AMERICA ZIP: 20004
                                                                                                                                                                                                  RESULT 3
US-08-722-126A-6
; Sequence 6, Application US/08722126A
; Patent No. 6034227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFREENCE/DOCKET NUMBER: PECH
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEPHAX: (202) 737-3528
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
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WICEKUL 187
                                                                                         181 WICKKVL 187
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STRANDEDNESS: Si
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Best Local Similarity
                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
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PCT-US95-04258-6
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                                                                                                                                                            61 CCGSKGFMCSQCSRCPNLMMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLFFPDNQGVN 120
                                                                                                                                                                                                                                               CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                      LFGEYLGQDFYWIGLRNIDGWRWEGGPALSLRILTNSLIQRCGAIHRNGLQASSCEVALQ 180
                                                 1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL 60
                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MADNSIYSTLETPAAAPRVQDDSRWKVKAVLHRPCVSYLVWYALGLLTVILMSLLLYQRTL
                                                                       1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRRAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
        Gaps
        .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 81.4%; Score 838; DB 5; Length 188; Best Local Similarity 80.7%; Pred. No. 1.8e-86; Matches 15; Conservative 15; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
APPLICATION NUMBER: IL 109257
FILLING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
      21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A DNA MOLECULE ENCODING A MAST CELI
FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
        15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application PC/TUS9504258 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PECH:
TELECOMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEFX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
TITLE OF INVENTION: A DNA
TITLE OF INVENTION: FUNCT:
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              188 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 248633
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acid
        151; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 419 Sevent CITY: Washington STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                      WICKKVL 187
                                                                                                                                                                                                                                                                                                                                                 181 WICEKVL 187
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                                                                                                                                      61
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        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14 GTLGIİCLSLMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCQEKWVGYRC 70
                                                                                                                                                                      1 PSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCW
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                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       142 RWEGGPALSLRILTN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 179;
      25.9%; Score 267; DB 4; Length 76; 59.5%; Pred. No. 1.2e-22; ive 10; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hillman, Jennifer L.
APPLICANT: Au-Young, Janice
APPLICANT: Goll, Surya K.
APPLICANT: Goll, Surya K.
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17.3%; Score 178.5; DB 1;
31.8%; Pred. No. 3.5e-12;
iive 17; Mismatches 68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Incyte Pharmaceuticals, Inc
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTY: 0.5.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: Diskette
COMPUTER: EastSEQ Version 1.5
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,095
FILING DATE: Filed Herewith
ATTORNEY, AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0110 US
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Sequence 9, Application US/08690095; Patent No. 5792648
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                                                                                                                                                                                                                                                      133 IGLRNIDGWRWEGG 146
                                                                                                                                                                                                                                                                                                                61 IGLRNMSGWRWEDG 74
   Query Match
Best Local Similarity 59.5*
Matches 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS
LENGTH: 179 amino acio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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Best Local Similarity
Matches 54; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: 3174 Por
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LIBRARY: General Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Commercial Comme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             US-08-690-095-9
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US-09-531-056A-23

US-09-531-056A-23

Sequence 23, Application US/09531056A

Patent No. 6455683

GENERAL INFORMATION:

APPLICANT: Bitstol-Wyers Squibb Company

TITLE OF INVENTION: PROTEINS

FILE REFERENCE: DB20 NP

CURRENT PALLICATION NUMBER: US/09/531,056A

CURRENT PALLING DATE: 2000-03-20

NUMBER OF SEQ ID NOS: 24

SOFTWARE: Patentin version 3.0

LENGTH: 76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQBYVGEDFYWIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 LRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVL 113
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                                                                                                                                                                                                                                                                                                                                                                Score 551; DB 5; Length 114;
Pred. No. 2e-54;
9; Mismatches 9; Indels
                                                                                      A DNA MOLECULE ENCODING A MAST CELL
FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                TITLE OF INVENTION: A DNA MOLECULE ENCODING A MA
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN
NUMBER OF SEQUENCES: 10
CORRESSED ANDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Mashington
STATE: D.C.
Sequence 6, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKGT NUMBER: PE
TELECOMOUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 53.5%;
Best Local Similarity 84.1%;
Matches 95; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein PCT-US95-04258-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
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Matches 54; Conservative
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linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLONE: 1098616
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-688-342-3
                                                                                         CITY: P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 NCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEEHTAW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KDSTCSHCPSCPILWTRNGS 84
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 17.3%; Score 178.5; DB 2; Length 179; Best Local Similarity 31.8%; Pred. No. 3.5e-12; Matches 54; Conservative 17; Mismatches 68; Indels 31
                                                                    GENERAL INFORMATION:
APPLICANT: Chang, Chiwen
APPLICANT: Aramburu Beltran, Jose
APPLICANT: Lopez-Botet, Miguel
APPLICANT: Lopez-Botet, Miguel
APPLICANT: Lanier, Lewis L.
TITLE OF INVENTION: Purified Mammalian NK Antigens and TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,578
                                                                                                                                                                                                                        STREET: DNAX Research Institute STREET: 901 California Avenue CITY: Palo Alto STATE: California COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,339
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/OCCET NUMBER: DX0391
TELECOMMINICATION:
TELEPHONE: 415-852-9196
                                                                                                                                                                                                                                                                                                                                                                ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBB PC compatible
OPBRATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 3, Application US/08688342
Patent No. 5871964
GENBRAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Gocks, Benjamin G.
APPLICANT: Goli, Surya K.
                                  Sequence 2, Application US/08650578 Patent No. 5811284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 GLLTVILMSLLMYQRILCCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 179 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-650-578-2
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RESULT 7
US-08-650-578-2
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85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID----GW 141
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -KDSTCSHCPSCPILWTRNGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2; Length 179;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.3%; Score 178.5; DB 2;
31.8%; Pred. No. 3.5e-12;
tive 17; Mismatches 68;
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FASTERO VESSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/68,342
FILING DATE: F11ed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: 36,749
REPERENCE/DOCKET NUMBER: PF-0095-1 CIP
TELEPHONE: 415-855-0555
TELEPHONE: 415-855-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-113-788-3; Sequence 3, Application US/09113788; Patent No. 5969104
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ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
THEORY TOWNS TOWNSTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94304
COMPUTER READABLE FORM:
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85 HCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDFYWIGLRNID---GW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         71 NCYFISSEQKTWNESRHLCASOKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEEHTAW 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14 GTLGIICLSLMATLGILLKNSFTKLSIEPAFTPGPNIELQKDSDC--C-SCOEKWVGYRC 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----KDSTCSHCPSCPILWTRNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 RWEGGPALSLRILIN---SLIQRCGAIHRNG-LQASSCEVALQWICKKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 LWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                 ch 17.3%; Score 178.5; DB 3; Length 179; 1. Similarity 31.8%; Pred. No. 3.5e-12; 54; Conservative 17; Mismatches 68; Indels 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08722126A
Patent No. 603427
GENERAL INFORMATION:
APPLICANT: BCERT, Israel
APPLICANT: GUTHWANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATE: US/08/722,126A FILING DATE: 08-OCT-1996
                     ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 9F-0110 US
REFERENCE/DOCKET NUMBER: 9F-0110 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-85-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
STRANDENNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT/US95/04258
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44 GLLTVILMSLLMYQRILCCGS-
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APPLICATION NUMBER: PCT/US
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109
                                                                                                                                                                                                                                                                         TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                       GenBank
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LIBRARY: Genu-
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US-08-722-126A-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Au-Young, Janice
APPLICANT: Goli, Surya K.
TILLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17.3%; Score 178.5; DB 2;
31.8%; Pred. No. 3.5e-12;
tive 17; Mismatches 68;
                                                                                                      APPLICATION
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/688,342
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 95,749
REGISTRATION NUMBER: PF-0095-1 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-655-055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
TWATH : 179 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                   US/09/113,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,789
                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/00/11-
PRIOR APPLEMENT NUMBER: US/00/11-
PRIOR APPLEMENT NUMBER: US/00/11-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9, Application US/09113789 Patent No. 6034219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44 GLLTVILMSLLMYQRILCCGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                STRAND.
TOPOLOGY: linear
MOLECULE TYPE: peptide
IMMEDIATE SOURCE:
LIBRARY: GenBank
ATONE: 1098616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54; Conservative
Diskette
                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 54; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 3174 Por
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             U.S.
  MEDIUM TYPE:
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75 CPILWIRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLIFFPDNQGVKLFGEYLGQDFYWIG 134
                                                                                               75 CPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLIFPDNQGVKLFGBYLGQDF--YW 132
                                                                                                                                                                                       133 IGLRNI---DGWRWEGGPALS---LRILTNSLIQRCGAIHRNGLQASSCEVALQWICKKV 186
                                                                                                                                                                                                                       61 IGLRYTLPDMNWKWINGSTLNSDVLKITGDTENDSCAAISGDKVTFESCNSDNRWICQKE 120
                                                                                                                             1 CSEDWVGYQRKCYPISTVKRSWTSAQNACSEHGATLAVIDSEKDMNFLKRYAGREEHWVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Gaps
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14.8%; Score 152; DB 5; Length 122; 27.9%; Pred. No. 2e-09; tive 22; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: PECHT, Israel
APPLICANT: GUTHWAN, MARCELO D.
APPLICANT: GUTHWAN, MARCELO D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAPA)
NUMBER OF SECUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

COMPUTER: Floppy disk

APPLICATION NUMBER: PCT/US95/04258

FILING DATE: 06-APR-1995

PILING DATE: 06-APR-1995

PILING APPLICATION NUMBER: IL 109257

FILING DATE: 08-APR-1994

ATTOMENYAGENT: INFORMATION:

ANDER APPLICATION NUMBER: IL 109257

FILING DATE: 08-APR-1994

ATTOMENYAGENT: INFORMATION:

ANDER APPLICATION NUMBER: IL 109257

FILING DATE: 08-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14.6%; Score 150.5; DB 3; 26.3%; Pred. No. 2.8e-09; iive 20; Mismatches 59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington STATE: D.C. COUNTRY: UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 8, Application US/08722126A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: BROWDY, ROGER L.
RRGISTRATION UNDBER: 25,618
REFERENCE/DOCKET NUMBER: PECHT
TELECOMMUNICATION INFORMATION:
TELEPRAN: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              115 amino acids
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Best Local Similarity 26.3%
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                     34; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
       Query Match
Best Local Similarity
Matches 34; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6034227
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                         187 LY 188
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US-08-722-126A-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       133 IGLRNI----DGWRWEGGPALS---LRILINSLIQRCGAIHRNGLQASSCEVALQWICKKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 IGLRYTLPDMNWKWINGSTLNSDVLKITGDTENDSCAAISGBKVTFESCNSDNRWICQKE 120
                                                                                                                                                                                                                                                                                                                                                                                                                                               1 CPQDWLSHRDKCFHVSQVSNTWEEGLVDCDGKGATLMLIQDQEELRFLLDSIKEKKNSFW 60
                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                   .
8
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                                                                                                                                                                                                                                                                                                                  Query Match 14.8%; Score 152; DB 3; Length 12:
Best Local Similarity 27.9%; Pred. No. 2e-09;
Matches 34; Conservative 22; Mismatches 58; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 9, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: PUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06.APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08.APR-1994
ATTORNEY/BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E: BROWDY AND NEIMARK
419 Seventh Street, N.W., Suite 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PECHT=1 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-2197
TELEFAX: 202-737-3528
              REFERENCE/DOCKET NUMBER: PECHT=1A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                               TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 122 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  122 amino acids
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
                                                                                                                                                                                                    single
                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
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STREET: 41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 CSEDWVGYQRKCYFISTVKRSWTSAQNACSEHGATLAVIDSEKDMNFLKRYAGREEHWVG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                             61 LKKEPGHPWKWSNGKEFNNWFNVTGS--DKCVFLKNTEVSSMECEKNLYWICNK 112
135 LRNIDG--WRWEGGPALSLRI-LTNSLIQRCGAIHRNGLQASSCEVALQWICKK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        135 LRNIDG--WRWEGGPALSLRI-LTNSLIQRCGAIHRNGLQASSCEVALQWICKK 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 5; Length 115;
                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
RAPPLICATION NUMBER: II 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     59; Indels
                                                                                                                                                                                                      A DNA MOLECULE ENCODING A MAST CELL
FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14.6%; Score 150.5; DB 5 26.3%; Pred. No. 2.8e-09; tive 20; Mismatches 59
                                                                                                                                                                                                                                                                                   ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PECHT=1 PCT
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Fatent No. 6262244
GENERAL INFORMATION:
TITLE OF INVENTION: DNA and amino ac
TITLE OF INVENTION: natural killer of INVERS SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Michael W. Glynn
                                                                                                                                          Sequence 8, Application PC/TUS9504258 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REPERROCE/DOCKET NUMBER: PECH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEPHONE: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: 248633
INFORMATION FOR SEQ ID NO: 8 SEQUENCE CHARACTERISTICS:
LENGTH: 115 amin
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amino acid
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MOLECULE TYPE: protein
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                    TITLE OF INVENTION: A
TITLE OF INVENTION: FU
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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Best Local Similarity
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US-08-543-246B-19
                                                                                                      RESULT 14
PCT-US95-04258-8
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71 HCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVKLFGEYLGQDF 130
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                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRINARE: Patentin Release #1.0, Version #1.30 (EPO)
APPLICATION NUMBER: US/08/543,246B
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14.2%; Score 146; DB 3; 28.9%; Pred. No. 1.1e-08; iive 18; Mismatches 62,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118-7704/PCT/CONT
No. 6262244artis Corporation
                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER:
US 07/676,663
FILING DATE: 28-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02469
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/122,514
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search completed: August 10, 2004, 16:45:20 Job time : 15.5 secs
                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 24-5EP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Kassenoff, Melvyn M.
REGISTRATION NUMBER: 26,389
REFERENCE/DOCKET NUMBER: 118-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-522-6927
               564 Morris Avenue
                                                                                                                               Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          135 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 28.9*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-terminal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
                                                                    COUNTRY: US
ZIP: 07901-1027
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amino acid
ADDAL
STREET: SUMMIT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'RAGMENT TYPE:
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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- protein search, using sw model OM protein

Run on:

August 10, 2004, 16:39:40; Search time 13.5 Seconds (without alignments) 1339.556 Million cell updates/sec

Perfect score:

US-09-811-367B-5 1036 1 MADNSIYSTLELPAAPRVQD......GLEASSCEVALQWICEKVLP 188 Seguence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 283366 seqs, 96191526 residues Searched:

95185

Minimum DB seg length: 0 Maximum DB seg length: 188

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database

PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	ption	mast cell function			adkisacutacin beta	hepatic lectin hom	alpha	coadulation factor	botrocetin alpha c	botrocetin beta ch		coaqulation factor	ackisacutacin alph	hepatic lectin hom	lectin BRA3-2 pred				coadulation factor	regenerating islet	pancreatic stone p		lectin, galactose-	pancreatic stone n	echicetin heta cha	coadulation factor	regenerating jalet		red II. redeperati	pancreatitis-assoc
SUMMARIES	ID	I59421	T28140	T28141	JC7135	WMVZF2	PC7027	JC4691	A47267	B47267	JC7105	B42972	JC7134	WMVZF8	LNRC3	LNRC1	S78774	A49616	JC4329	RGHU1A	A45751	JC5059	A38609	A28351	JC2415	JC4690	RGHU1B	529822	B47148	854979
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	Length	188	170	156	146	167	144	146	133	125	146	123	152	116	162	162	155	175	129	166	166	125	135	165	123	152	166	175	173	174
040	Query	100.0	15.7	15.3	14.1	13.2	13.0	12.3	•		11.7	11.1	11.1	10.9	10.9	10.8	10.5	10.0	6.6	9.6			•	9.5	•		•	9.1	9.1	•
	Score	1036	162.5	158	146	137	134.5	127.5	a	123.5	121.5	115	114.5	113	112.5	112	108.5	103.5	102.5	102	0	100.5	100	86	96.5	96.5	95	94.5	94	92.5
ŗ	Kesult No.	1	7	ю	4	S	9	7	60	ð	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29

pancieatic stone p	antifreeze protein	bitiscetin alpha c	pancreatic thread	type II antifreeze	hypothetical profe	lectin - barnacle	tokaracetin beta c	echinoidin = sea n	red T redeneration	antifreeze protein	ovocleidin - chick	hepatic lectin hom	regenerating prote	hypothetical prote	alboaggregin-B alp
A41719	A34313	JC5058	A37194	JC7938	T21396	S10548	S56007	A26697	A47148	JH0626	278596	WMVZEL	183377	T28809	B56829
7	н	N	N	7	7	7	7	7	7	Н	7	н	N	N	0
175	163	131	175	147	153	173	40	147	165	175	142	143	174	166	40
6.8	8.8	9.8	8.5	8.4	8.4	8.4	8.3	8.2	7.9	7.9	7.9	7.9	7.6	7.6	7.4
92	91	89.5	88	87	87	87	98	85	82	82	81.5	81.5	79	78.5	77
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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C. Accession: 159421
R;Guthmann, M.D.; Tal, M.; Pecht, I.
R;Guthmann, M.D.; Tal, M.; Pecht, I.
R;Guthmann, M.D.; Tal, M.; Pecht, I.
Proc. Natl. Acad. Sci. U.S.A. 92, 9397-9401, 1995
A,Title: A secretion inhibitory signal transduction molecule on mast cells is another of A,Reference number: 159421; MUID:96016176; PMID:7568140
A,Recession: 159421
A,Recession: ISP421
A,Residues: preliminary; translated from GB/EMBL/DDBJ
A,Molecule type: mRNA
A,Residues: 1-188 < RES>
A,Residues: 1-188 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LFQEYVGEDFYWIGLRDIDGWRWEDGPALSISILSNSVVQKCGTIHRCGLHASSCEVALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X79812; NID:g1020141; PIDN:CAA56208.1; PID:g1020142 C;Genetics:
                                        mast cell function associated antigen - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Uul-1996 #sequence_revision 02-Uul-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MADNSIXSTLELFRAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 100.0%; Score 1036; DB 2; Best Local Similarity 100.0%; Pred. No. 3.2e-90; Matches 188; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               181 WICEKVLP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181 WICEKVLP 188
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RESULT 1
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RESULT 2 T28140

natural killer cell receptor homolog - chicken (fragment)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T28140
R;Milne, S:; Kaufman, J:; Beck, S:
Submitted to the EMBL Data Library, May 1998
A;Poescription: DNA sequencing and analysis of the chicken major histocompatibility comp A;Reference number: Z20475
A;Accession: T28140
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA

9

98 48

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C;Species: fowloox virus
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C;Date: 30-Sep-1988 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C;Accession: B29963
A;Title: Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment of fowlpo A;Reference number: J70442; MUID: 88229622; PMID: 2836548
A;Accession: B29963
A;Accession: B29963
A;Accession: B29963
A;Resiques: 1-167 < TOM>
A;Resiques: 1-167 < TOM>
A;Resiques: 1-167 < TOM>
A;Cross-references: GB:D00295; NID: g221380; PIDN: BAA00192.1; PID: g221383
C;Keywords: early protein
F;49-152/Domain: C-type lectin homology <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aggretin alpha chain - Malayan pit viper (fragment)
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Accession: PC7027
R;Chung, C.H.; Au, L.C.; Huang, T.F.
B;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem. Biophys. Res. Commun. 263, 723-727, 1999
A;Title: Molecular cloning and sequence analysis of aggretin, a collagen-like platelet A;Reference number: PC7027; MUID:99443731; PMID:10512747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 SLKFCAD--KGSHLLTFPDNQG----VNLFQEYVGEDFYWIGLRDI-DG--WRWEDGPAL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95 DWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSIL 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   69 NWNDSKKLCDVWDSSLIRFDNIETLNFVSRY-GKGSYWI---DINQNRKIPGINFSL-YY 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - fowlpox virus (isolate HP-438[Munich])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35 VSYLVMVALGLLTVILMSLILLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 VSCYALTVLGILCLILFTILV---VVTCKWYYAPPYFSKVCPDEWIGYNSKCYYFTINET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39 VMVALGLLIVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ----LSGTAADCPSEWSSYEGHCYKPFDEPKTWAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                             A,Accession: PCOCCESSION: PCOCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 13.2%; Score 137; DB 1; Le
1 Similarity 29.1%; Pred. No. 1.2e-05;
44; Conservative 21; Mismatches 78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 146; DB 2;
Pred. No. 1.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 SNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 EQGVNDICLLFDTSNIIEMSCIFHERTICVK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DYKDWREQFECLVSRIVNNEWLSMDCGT 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -SLSILSNSVVQKCGT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hepatic lectin homolog (BamHI-ORF2)
                                            A; Experimental source: venom gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.18;
27.78;
A; Cross-references: GB: AF176421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5 IFVSFGLLVVFLS----
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Best Local Similarity
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Best Local S
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C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Species: Agkistrodon acutus (sharp-nosed viper)
C;Accession: JC7135; Pc7038
B;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
B;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
B;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
B;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
B;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
B;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
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B;Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.
B;Cheng, X.; Qian, Y.; Liu, Q.; Liu, B.X.Y.; Zhang, M.; Liu, J.
B;Cheng, X.; Qian, Y.; Liu, Q.; Liu, B.X.Y.; Zhang, M.; Liu, J.
B;Cheng, X.; Qian, Y.; Liu, Q.; Liu, B.X.Y.; Zhang, M.; Liu, J.
B;Cheng, X.; Qian, Y.; Liu, Q.; Liu, B.X.Y.; Zhang, M.; Liu, J.
B;Cheng, X.; Qian, Y.; Liu, Q.; Liu, B.X.Y.; Zhang, M.; Liu, J.
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B;Cheng, X.; Qian, Y.; Liu, Q.; Liu, B.X.Y.; Zhang, M.; Liu, J.
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B;Cheng, X.; Qian, Y.; Liu, Q.; Liu, B.X.Y.; Zhang, M.; Liu, J.
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B;Cheng, X.; Qian, Y.; Liu, Q.; Liu, B.X.Y.; Zhang, M.; Liu, J.
B;Cheng, X.; Qian, Y.; Liu, Quin, M.; Liu, M.; Liu, J.
B;Cheng, X.; Qian, Y.; Liu, Qian, M.; Liu, M.; Liu, Qian, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.; Liu, M.
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R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, J.; Beck, S.

R/Milne, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman, S.; Kaufman,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132 WIGLRDIDG----WRWEDGPALS--LSILSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                  A;Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292544; PIDN:CAA18960.1
A;Experimental source: clone cB12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 CSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47 CLLCPQFWRLLGDRCYELSTEKGNWTQAKMKCENLQSQLAVLRKKAEEDHLQQMAGAEPV 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             132 WIGLR-DIDGWRWEDGPAL----SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C type lectin, B locus - chicken
C;Species: Gallus gallus (chicken)
C;Spate: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 170;
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A;Note: Intron positions not resolved (incomplete sequence)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Score 162.5; DB 2; Pred. No. 4.8e-08; 16; Mismatches 60
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28.1%;
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Best Local Similarity 28.1%
Matches 34; Conservative
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A,Map position: 16
A,Introns: 17/1; 74/3; 110/2
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Best Local Similarity
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botrocetin alpha chain - jararaca
N'Alternate names: two chain botrocetin alpha chain
C;Species: Bothrops jararaca (jararaca)
C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Accession: A47267; B37958
C;Accession: A47267; B37958
A;Tosanh, Y.; Fulimura, Y.; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator physical controls of two-chain botrocetin, a von Willebrand factor modulator physikeference number: A47267; MUID:93157385; PMID:8430107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Note: sequence extracted from NCBI backbone (NCBIP:124085)
Frulimura, Y: Titani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Su;
Biochemistry 30, 1957-1964, 1991
A;Title: Isolation and chemical characterization of two structurally and functionally do
A;Reference number: A37958; MUID:91129280; PMID:1993206
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A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: protein
A, Molecule type: Trotein
A, Moleci sequence extracted from NCBI backbone (NCBIP:124086)
B, Note: sequence extracted from NCBI backbone (NCBIP:124086)
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C;Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 15-May-1998
C;Datesession: B47267; C37958
R;USami, Y:; Fulfimura, Y:; Suzuki, M.; Ozeki, Y.; Nishio, K.; Fukui, H.; Titani, K.
Proc. Natl. Acad. Sci. U.S.A. 90, 928-932, 1993
A;Title: Primary structure of two-chain botrocetin, a von Willebrand factor modulator
A;Reference number: A47267; MUID:93157385; PMID:8430107
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A;Residues: 1-40 <FUJ>
C;Complex: hetrancdimer of alpha (see PIR:A47267) and beta chains
C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hemagglutinin; heterodimer; venom
                                 : : | : |::||
--WRSRACRMMAQFVCE 143
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                                 LRYKAWAEESYCVYFKSTNNK-
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A,Residues: 1-133 <USA>
A,Experimental source: venom
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Matches 30; Conserv
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Coagulation factor IX/factor X-binding protein chain A precursor - habu
C; Species: Trimeresurus flavoviridis (habu)
C; Coession: 16-401-1996 #sequence revision 16-Aug-1996 #text_change 20-Jun-2000
C; Accession: JC4691; B39332; JC4330 In 16-Aug-1996 #text_change 20-Jun-2000
C; Accession: JC4691; B39332; JC4330 In 1996
A; Matsuzaki, R.; Yoshiara, E.; Yamada, M.; Shima, K.; Atoda, H.; Morita, T.
A; Title: cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from s A; Reference number: JC4690; MUID:96184662; PMID:8645314
A; Accession: JC4691
A; Molecule type: mRNA
A; Residues: 1-146 <AMAI:
A; Experimental source: venom
R; Accession: JC4691
A; Title: The primary structure of coagulation factor IX/factor X-binding protein isolate
A; Reference number: A39332; MUID:91332000; PMID:1831197
A; Residues: 24-146 <ATO:
A; Residues: 24-146 <ATO:
B; Atoda, H.; Ishikawa, M.; Yoshihara, E.; Sekiya, F.; Morita, T.
B; Biodem: H19, 965-973, 1993
A; Midlem: H2, 965-973, 1993
A; Title: The primary structure of coagulation factor immunoglobulin B.
A; Reference number: A39332; MUID:91332000; PMID:1831197
A; Residues: 24-146 <ATO:
B; Accession: B39332
A; Midle ATO:
B; Accession: B39332
A; Midle ATO:
B; Accession: B39332
A; Midle ATO:
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A;Reference number: JC4329; MUID:96318509; PMID:8749314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99 SLKFCADK--GSHLLTFPDNQGVNL----FQEYVGEDFYWIGLRDI----DGWRWEDGPA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CDFGWSPYDQHCYQAFNEQKTWDEAEKFCRAQENGAHLASIESNGEADFVSWLISQKDEL 72
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A. Mocession: UC4330
A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
A. Molecule type: protein
C. Keywords: anticoagulant; blood coagulation; lectin; venom
C. Keywords: anticoagulant; blood coagulation; lectin; venom
C. Keywords: anticoagulant; blood coagulation; lectin; venom
C. Keywords: anticoagulant; blood coagulation; lectin; venom
C. Keywords: factor IX/X binding protein chain B #status predicted cMAT>
F.25-142/Domain: C-type lectin homology cLCH>
F.25-142/Domain: C-type lectin homology status predicted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFC--ADKGSHLLTFPDNQGVNLF---
                                                                                                                                                                                                                                                                                                 Length 144;
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                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          149 L-----SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICE 184
                                      A, Residues: 1-144 <CHU>
A, Experimental source: venom gland
C, Superfamily: tetranectin; C-type lectin homology
C, Keywords: disulfide bond; platelet aggregation; venom
                                                                                                                                                                                                                                                                                  13.0%; Score 134.5; DB 2; 28.0%; Pred. No. 1.7e-05; ive 19; Mismatches 57;
                                                                                                                                                                                                                             Query Match
Best Local Similarity 26...
37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         177 VALQWICEKVLP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        133 QMHAFVC-KLLP 143
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A; Molecule type: mRNA
A; Residues: 1-144 < CHU>
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Agk Bacutacian Appea chair precursor: a marp-inced viper.

Agk Bacutacian Appa chair precursor: a marp-inced viper.

C; Species: Agkistrodon acutus (sharp-nosed viper)

C; Species: Agkistrodon acutus (sharp-nosed viper)

C; Accession: U7(134; PC7037

C; Accession: U7(134; PC7037

R; Cheng, X.; Qian, Y.; Liu, Q.; Li, B.X.Y.; Zhang, M.; Liu, J.

R; Cheng, Res. Commun. 265, 530-535, 1999

A; Title: Purification, characterization, and cDNA cloning of a new fibrinogenlytic veno A; Reference number: U7(134; MUID:20025379; PMID:10558903

A; Accession: U7(134; MUID:20025379; PMID:10558903

A; Residues: 1-152 cCHE>

A; Residues: 1-152 cCHE>

A; Experimental source: venom gland

A; Accession: PC7037

A; Accession: PC7037

A; Molecule type: protein

A; Residues: 24-53;84-86;87-94;125-136;137-152 cCH2>

C; Superfamally: tetranectin; C-type lectrin homology

C; Superfamally: tetranectin; C-type lectrin homology

C; Superfamally: tetranectin; C-type lectrin homology

C; Superfamally: advantation alpha chain #status experimental cMAT>

F; 24-152/ Product: agkisacutacin alpha chain #status experimental
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C; Species: fowlpox virus
C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C; Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 16-Jun-2000
C; Date: 30-Sep-1989 #sequence analysis of an in.2 kilobase, near-terminal, BamHI fragment of fowlpc 3. Gen. Virol. 69, 1025-1040, 1988
A; Title: Sequence analysis of an in.2 kilobase, near-terminal, BamHI fragment of fowlpc A; Reference number: JT0442; MID:88229622; PMID:2836548
A; Recession: H29963
A; Accession: H29963
A; Residues: 1-116 < TCM>
A; Residues: 1-116 < TCM>
A; Residues: 1-116 < TCM>
A; Cross-references: GB:D00295; NID:G221380; PIDN:BAA00203.1; PID:G221394
C; Superfamily: Gwlpox virus hepatic lectin homolog; C-type lectin homology
C; Keywords: early protein
F; 48-116/Domain: C-type lectin homology #status atypical < LEC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 SIKFCADK--GSHILITFPDNQGVNLFQEYVGEDF-----YWIGIRDID-----GWRWED 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  49 AESFCTKQVNGGHLVSIESSGEADFVAHLIAQKIKSAKIHVWIGLRAQNKEKQCSIEWSD 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        39 VMVALGLLIVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNS 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----LSGTAADCSSGWSSYEGHCYKVFKQSKTWAD 48
                                                                                                                                                                                                   hepatic lectin homolog (BamHI-ORF8) - fowlpox virus (isolate HP-438[Munich])
                                                                                                                                                    75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCAD--KGSHLLITFPDNQG----VNLFQEYVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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11.1%; Score 115; DB 2; Length 123; 33.8%; Pred. No. 0.001; tive 12; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GPALSLSILSNSVVQKCGTIH-RCGLHASS---CEVALQWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              agkisacutacin alpha chain precursor - sharp-nosed viper
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11.1%; Score 114.5; DB 2; 21.5%; Pred. No. 0.0014; tive 22; Mismatches 73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
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                                                                                                                                                                                                                                                                                                                129 DEYWIGLRDIDGWRWED 145
                                                                                                                                                                                                                                                                                                                                                                               64 PATWIGL----GNMWKD
                                                                                     26; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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hes 35; Conserv
                                              Similarity
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Best Local Si
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           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   aggretin beta chain - Malayan pit viper
C;Species: Calloselasma rhodostoma (Malayan pit viper)
C;Species: Oalbec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C;Accession: 05-Dec 1999
B;Chung, C.H.; Au, L.C.; Huang, T.F.
Biochem: Biophys. Res. Commun. 263, 733-727, 1999
A;Title: Molecular cloning and sequence analysis of aggretin, a collagen-like platelet A;Reference number: PC7027; MUID:99443731; PMID:10512747
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R. Takeya, H.; Nishida, S.; Miyata, T.; Kawada, S.; Saisaka, Y.; Morita, T.; Iwanaga, S.
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J. Biol. Chem. 267, 14109-14117, 1992
A. Thile: Coaqulation factor X activating enzyme from Russell's viper venom (RVV-X). A r
A; Reference number: A42972; MUID:92332516; PMID:1629211
A; Reference number: A42972
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C,Date: 04-Mar_1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SLKFC--ADKGSHLLTFPDNQG----VNLFQEYVGEDFYWIGLRDI---DGWRWEDGPAL 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 AERFCKIQPKHSHIVSFQSAEEADFVVKITRPRIKANIVWMGISNIWHGCNWQWSDGARL 108
                                                                                                                                                                                                                                                                                                                    75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADK--GSHLLITFPDNQGVNLFQEYVGE---- 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ---LSGTGADCPSGWSSYEGHCYKPFNEPKNWAD 48
                                                                                                                                                                                                                                                                                                                                                                   2 CPPDWSSYEGHCYRFFKEWMHWDDAEEFCTEQQTGAHLVSFQSKEEADFVRSLTSEMLKG 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39 VMVALGLITVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNS
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                                                                                                                                                                                                                                              13;
                   F;2-121/Domain: C-type lectin homology <LCH>
F;2-13,30-121,98-113/Disulfide bonds: #status experimental
F;75/Disulfide bonds: interchain (to alpha-80) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11.7%; Score 121.5; DB 2; Length 146; 23.3%; Pred. No. 0.0003; ive 24; Mismatches 65; Indels 33
                                                                                                                                                                           Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A,Molecule type: mRNA
A,Residues: 1-146 <CHU>
A,Experimental Source: venom gland
C;Superfamily: tetranectin; C-type lectin homology
C;Superfamily: tetranectin; platelet aggregation; venom
                                                                                                                                                                Score 123.5; DB 2;
Pred. No. 0.00016;
2; Mismatches 32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            129 DFYWIGLRDIDGW-----RWEDG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DVVWIGLSDV--WNKCRFEWTDG 82
                                                                                                                                                                                                                                                  12;
                                                                                                                                                                11.9%; S
nilarity 31.3%; P
Conservative 12;
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                                                                                                                                                                    Query Match
Best Local Similarity
Matches 26; Conserv
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Best Local Similarity

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A,Molecule type: protein
A,Rolecule type: protein
A,Rolecule type: 27-145, K',147-162 cMUR>
A,Role: 146-Arg was also found
C,Comment: This galactose-binding lectin is isolated from the coelomic fluid.
C,Comment: This protein plays important roles in defense mechanisms and in development
C,Comment: The molecule is a tetramer of identical chains.
                                      A,Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.
A,Reference number: A26094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 NDAQLACQTVHPGAYLATIQSQLENAFISETVSNNRLWIGLNDIDLEGHYVWSNGEATDF 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97 NSSLKFC--ADKGSHLLITFPDNQGVNLFQEYVGEDFYWIGLRDID----GWRWEDGPALSL 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 VMVALGLLTVILMSLLLYQRTLCCGSKGFMCSQCSRCP-NL-WMRNGSHCYYFSMEKRDW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -- AITTGECT-CPGNLDWQEYDGHCYWASTYQVRW
                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: tetranectin; C-type lectin homology
C;Keywords: hemolymph; homotetramer; lectin
F;L-24Domain: signal sequence #status predicted <SIG>
F;25-162/Product: lectin BRA3-1 #status experimental <MAT>
F;26-150/Domain: C-type lectin homology cLCH>
F;26-150/Domain: C-type lectin homology eLCH>
F;26-35-56-150/Isulfide bonds: #status experimental
F;157/Disulfide bonds: interchain (to 160) #status experimental
F;160/Disulfide bonds: interchain (to 157) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 10.8%; Score 112; DB 1; Best Local Similarity 26.4%; Pred. No. 0.0026; Matches 37; Conservative 17; Mismatches 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search completed: August 10, 2004, 16:44:40 Job time : 13.5 secs
            Biophys. Acta 874, 285-295, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : | | : : 110 TYWSSNNPNNWENQDCGVVN 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            152 SILS-----NSVVQKCGTIH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :: |: |! |:
IVQAVTLLVVVF---
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                                                                                                   A; Accession: A26094
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and in development
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C;Date: 31-Dec-1988 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C;Accession: JC1504; Az6094
R;Takamatsu, N; Takeda, T:; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba, Gene 128, 251-255, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A,Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure
A,Reference number: JC1503; MUID:932994; PMID:8514190
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C;Date: 24-Feb-1994 #sequence_revision 09-Sep-1994 #text_change 16-Jul-1999
C;Accession: JC1503; A26094
E;Takamatsu, M.; Takeda, T.; Kojima, M.; Heishi, M.; Muramoto, K.; Kamiya, H.; Shiba, Gene 128, 251-255, 1993
A;Title: Acorn barnacle Megabalanus rosa lectin (BRA-3): cDNA cloning, gene structure. A;Reference number: JC1503; MUID:9329994; PMID:8514190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A,Molecule type: mRNA
A,Residues: 1-162 - ThXt>
R:Muxamoto, K.; Kamiya, H.
Biochim. Biophys. Acta 874, 285-295, 1986
A,Title: The amino-acid sequence of a lectin of the acorn barnacle Megabalanus rosa.
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                                                                                             --LLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGS 84
                                                                                                                                                          --CKEGWVGYNK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
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                                      Gaps
                                                                                                                                                                                                             HCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDID 139
                                                                                                                                                                                                                                                    A,Molecule type: protein
A,Molecule type: protein
A,Molecule type: protein
A,Molecule type: protein
A,Molecule type: protein
A,Molecule type: protein plays important roles in defense mechanisms and
C,Comment: This protein plays important roles in defense mechanisms and
C,Comment: The molecule is a tetramer of identical chains.
C,Superfamily: tetranectin, C-type lectin homology
C;Keywords: hemolymph; homotetramer; lectin
F;1-24/Domain: signal sequence #status predicted <SIG>F;25-1627 product: lectin BRA3-2 #status experimental <AMT>F;26-150/Domain: C-type lectin homology v.LCH>F;26-150,125-142/pisulfide bonds: #status experimental
F;16-39,56-150,125-142/pisulfide bonds: #status experimental
F;160/Disulfide bonds: interchain (to 160) #status experimental
                                      28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 VGEDFYWIGLRDID---GWRWEDGPALSLSILS-----NSVVQKCGTIH 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 162;
                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
22.6%; Pred. No. 0.0015;
ive 20; Mismatches 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                  precursor - barnacle (Megabalanus rosa)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lectin BRA3-1 precursor - barnacle (Megabalanus rosa)
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30.3%; Pred. No. 0.0023;
live 14; Mismatches 45
                                                                                                                                                    18 PCGS--IIIVLSVFVIILSTRPPVPPDIKILY--
                                                                                          PCVSYLVMVALGLLTVILMS-
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A; Molecule type: DNA; mRNA
A; Residues: 1-162 < TAK>
A; Cross-references: DDBJ: D13299
R; Muramoto, K.; Kamiya, H.
                            26; Conservative
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Best Local Similarity
Matches 33; Conserv
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7;

28; Gaps

58; Indels

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 10, 2004, 16:36:04 ; Search time 8 Seconds . :

(without alignments) 1223.649 Million cell updates/sec

US-09-811-367B-5 1036

1 MADNSIYSTLELPAAPRVQD......GLHASSCEVALQWICEKVLP 188 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

52070155 residues 141681 seqs, Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 188

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result		Ouery				
No.		Match		DB	ID	Description
Н	۱ (۲)	1	 	 H	CD94 MACMU	TIME CONTRACTOR SYSTEM
7	155			Н	CD94 HUMAN	013241 homo sapie
m	155			Н	CD94 PANTR	O9mz41 pan trogle
4	154			Н	V239_FOWPV	P14371 Fowlpox vi
2	153.5			Н	CLE2 HUMAN	092478 homo sanie
9	148.5	14.3	133	Н	RHCA_AGKRH	DR1397 ARKISTED
7	140.5			-	CVXB_CBODII	093427 crotalis
•				١,		COLEGE VALUE

	_	macaca mula	sapien	pan troglod	fowlpox_vir	sapien	agkistrodon	crotalus du	fowlpox vir	crotalus ho	aqkistrodon	agkistrodon	trimeresuru	bothrops ia	trimeresuru	bothrops ia		crotalus du	trimeresuru	haliotis la	aqkistrodon	trimeresuru	trimeresuru	sapien	mus musculu	homo sapien	echis carin	crotalus at	trimeresuru	pan troglod	rattus norv	homo sapien	echis carin	trimeresuru
	ption	maca	homo						£ow]								med				aqki	trin	trin	homo	mus	homc	echi	crot	trin	pan	ratt	homo	echi	trin
	Description	O9mzk9	013241	Q9mz41	P14371	092478	P81397	093427	P14370	P81509	Q9ygg9	Q9 <u>y19</u> 2	P23807	P22029	P81114	P22030	P07439	093426	P81113	P82596	P81398	P81116	P81111	006141	009049	P05451	P81017	P21963	P81112	Q95mi1	\sim	(T)	P81996	P23806
		34 MACMU	CD94 HUMAN	CD94 PANTR	39 FOWPV	32 HUMAN	A_AGKRH	CVXB CRODU	B_FOWPV	CHBB_CROHO	IA AGKHA	MMHB ACKHA	3 TRIFL	A BOTJA	14 TRIAB	BOTB BOTJA	33 MEGRO	CVXA CRODU	A3_TRIAB	HALLA	B AGKRH	3B_TRIAB	11_TRIAB	PAP1_HUMAN	3 MOUSE			CC_CROAT	ABA2 TRIAB	NKGF_PANTR	LITH_RAT	NKGF HUMAN	ECHB ECHCA	TRIFL
	ID	CD94	g	B	V239	CLE2	RHCA	S	ο Δ	B	MMHA	Ē	IXB	BOTA	ABA4	BQ.	Ë	S	AB	PLC	RHCB	ABBB	ABA1	PAI	PAP3	LITA	ECHA	LECG	ABZ	NK	E	NK	Ö	IXA
	DB	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	Н	7	Н	Н	Н	H	Н	-	Н	Н	7	Н	Н	Н	Н	Н	Н
	Length	179	7	7	163	4	133	148	167	117	157	146	146	133	123	125	162	158	125	155	129	118	131	175	^	9	133	co.	ന	N	9	158		152
* 0.10	Match	15.8			•	•	14.3	٠	•	2	N	S	12.3	N	3	ч	0	10.8	0	0	Ö		10.0		٠	•	٠	٠	٠	•	٠	•	٠	
	Score		155	155	154	153.5	148.5	140.5	137	132.5	131	130	127.5	126	124.5	123.5	113	111.5	109.5	109.5	107.5	106.5	103.5	103.5	103	102	101.5	100	99.5	98	86	97	96.5	96.5
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EMBL; AF190931; AAF74527.1; -. EMBL; AF190932; AAF74528.1; -.

Q9psm4 lachesis st P48304 homo sapien P3520 mus musculu Q08731 mus musculu Q9psn0 bitis ariet Q9ygpl trimeresuru P42854 rattus norv P17346 megabalanus P25031 rattus norv O09037 mus musculu P05140 hemitriper P81115 trimeresuru
LECG LACST LITB HUMAN PAP1_WOUSE LIT2 WOUSE LIT2 WOUSE LECG_BITAR LECG_RITAR PAP3_RAT LECG_MEGRO PAP1_RAT PAP1_RAT PAP2_MOUSE ANP_HEMAM ABBĀ_TRIAB
ппппппппппппппппппппппппппппппппппппппп
135 166 175 173 135 174 174 175 175
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ALIGNMENTS

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MEDLINE=20322487; PubMed=10866118;
LaBonte M.L., Levy D.B., Letvin N.L.;
"Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B, C, and D."; -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells.-!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family CD94 MACMU STANDARD; PRT; 179 AA.
CD94 MACMU STANDARD;
Q9MZK9; Q9GK91; Q9MZK7; Q9MZK8;
Q9MZK9; Q9GK91; Q9MZK7; Q9MZK8;
28-FEB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
10-OCT-2003 (Rel. 42, Last annotation update)
11-OCT-2003 (Rel. 42, Last annotation updat Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae, Name=3; Synonyms=CD94 alt; IsoId=Q9MZK9-3; Sequence=VSP 003054; -!- TISSUE SPECIFICITY: Natural killer cells. -!- SIMILARITY: Contains 1 C-type lectin family domain. members.
-!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- ALTERNATIVE PRODUCTS: Event=Alternative splicing; Named isoforms=3; Name=1; Synonyms=CD94-A; IsoId=Q9MZK9-1; Sequence=Displayed; Name=2; Synonyms=CD94-B; IsoId=Q9MZK9-2; Sequence=VSP_003055; SEQUENCE FROM N.A. (ISOFORM 1). MEDLINE=21158386; Pubmed=11261935; Immunogenetics 51:496-499(2000). Cercopithecinae; Macaca. NCBI TaxID=9544; RESULT 1 CD94 MACMU HID DESCRIPTION OF THE PROPERTY OF THE PROPERT

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                                                                                                                                                                                                  PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50641; C_TYPE_LECTIN_2; 1.
Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin; Alecrnative spliting; Polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                     SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD94 HUMAN STANDARD; PRT; 179 AA.
CD3241; O43321; O43773; Q9UBE3; Q9UBQ0;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
15-MAR-2104 (Rel. 43, Last annotation update)
16-MAR-2104 (Rel. 43, Last annotation update)
17-MAR-2104 (Rel. 43, Last annotation update)
18-MAR-2104                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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MEDLINE=98139529; PubMed=9472066;
Rodriguez A., Carretero M., Glienke J., Bellon T., Ramirez A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Lanier L.L.;
"Molecular characterization of human CD94: a type II membrane
glyoporotein related to the C-type lectin superfamily.";
Bur. J. Immunol. 25:2433-2437(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Score 163.5; DB 1; Length 179;
; Pred. No. 4.7e-09;
19; Mismatches 58; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-TYPE LECTIN (LONG FORM).
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                            EMBL; AF294886; AAG34498.1; -. HSSP; P22897; 1EGG.
InterPro; IPR001304; Lectin_C. Pfam; PF00059; lectin_G; 1. SMART; SM00034; CLECT; 1.
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EMBL; AF190933; AAF74529.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REDELINE=2238827; PubMed=12477932; Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Riausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Riausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Riausberg R.L., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K., Altschul S.F., Zeeberg B., Buttow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Schaefer C.B., Bonaldo M.F., Casavant T.L., Schaefer T.E., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schaefer T.E., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Vilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Blakesley R.W., Krzywinski M.I., Skalska U., Smailus D.E., Generation and initial analysis of more than 15,000 full-length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tadokoro K.,
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-!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HIA-E molecules by NK cells and some cytotoxic T-cells.
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                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=98267245; PubMed=9601951; Furukawa H., Yabe T., Watanabe K., Miyamoto R., Akaza T., 'Tohma S., Inoue T., Yamamoto K., Juji T.; "A alternatively spliced form of the human CD94 gene."; Immunogenetics 48:87-88 (1998).
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IsoId=Q13241-1; Sequence=Displayed;
Name=2; Synonyms=CD94.B;
IsoId=Q13241-2; Sequence=VSP_003053;
Name=3; Synonyms=CD94 alt;
IsoId=Q13241-3; Sequence=VSP_003052;
-:- TISSUB SPECIFICITY: Natural kiler. cells.
-:- SIMILANITY: Contains 1 C-type lectin family domain.
-:- DATABASE: NAME=PROW; NOTE=CD guide CD94 entry;
WWW="http://www.ncbi.nlm.nlh.gov/prow/cd/cd94.htm".
                                                                                                                                                                                                                                                                                     Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases
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-!- ALTERNATIVE PRODUCTS:
Lebrach H., Francis F., Lopez-Botet M.; "Structure of the human CD94 C-Type lectin gene."; Immunogenetics 47:305-309(1998).
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Y14288; CAA74663.1; JOINED.
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P14371, 09J500;
01-JAN-1990 (Rel. 13, Created)
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                                                              NKG2
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                             RG 90; GO:0004888; F:transmembrane; TAS.
RG 90; GO:0004888; F:transmembrane receptor activity; TAS.
RG 90; GO:0004888; F:transmembrane receptor activity; TAS.
RG 90; GO:0004688; F:transmembrane receptor activity; TAS.
RG 90; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
R 1nterPro; IPR001304; Lectin_C: 1.
R PRMIT; SM00034; CLECT; 1.
R PROSITE; F8000615; C_TYPE_LECTIN_1; FALSE_NEG.
R PROSITE; F8000615; C_TYPE_LECTIN_1; TANSMEMBRANE; Signal-anchor; Lectin;
R Alternative splicing; 3D-structure.
CYTOPLASME 1 1 CTYOPLASMIC (POTENTIAL).
T DOMAIN 1 1 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81 RNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 GYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99
                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
MAVFKTTLWRLISGTLGIICLSLMATLGILLKNS -> MAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24 WK-VKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFM--CSQCSRCPNLWM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | : : | | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         138 IDGWRWEDGPALSLSILSNSV---VQKCGTIHRCG-LHASSCEVALQWICEKVL 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
                                                                                                                                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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Khakoo S.I., Rajalingam R., Shum B.P., Weidenbach K., Flodin L.,
Muir D.G., Canavez F., Cooper S.L., Valiante N.M., Lanier L.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.0%; Score 155; DB 1; Length 179; 27.0%; Pred. No. 3.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1884D99E8D9583A7 CRC64;
                                                                                                                                                                                                                                                                                                                                   C-TYPE LECTIN (LONG FORM)
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEB-2003 (Rel. 41, Last sequence update)
10-0CT-2003 (Rel. 42, Last sequence update)
Natural killer cells antigen CD94 (NK cell receptor)
lectin-like receptor subfamily D, member 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (in isoform 2).
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BY SIMILARITY
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HGNC: 6378; KLRD1.
                                                                                                                                                                                                                                                                                                                 179
176
172
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 47; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9598;
                                                                                                                                                                                                                                                                                                                 32
98
61
89
152
83
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DISULFID
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g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF2byc., 1
HSSP, 192897, 126G.
InterPro; 192897, 1ectin_c; 1.

Pfam; PF00059; lectin_c; 1.

PROSITE; SM00034; CLECTI, 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

PROSITE; PS50041; C_TYPE_LECTIN_2; 1.

Alternative splicing.

CYTOPLASMIC (POTENTIAL).

SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

(POTENTIAL).

(POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81 RNGSHCYYFSMEKRDWNSSLKFCADKGSHLLIFPDNQGVNLFQEYVGEDFYWIGL---RD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14; Gaps
                                                                                                                                            -!- FUNCTION: Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells. -!- SUBUNIT: Can form disulfide-bonded heterodimer with NKG2 family
Shum B.P., Flodin L.R., Muir D.G., Rajalingam R., Khakoo S.I., Cleland S., Guethlein L.A., Uhrberg M., Parham P., "Conservation and variation in human and common chimpanzee CD94 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138 IDGWRWEDGPALSLSILSNSVV~--QKCGTIHRCG-LHASSCEVALQWICEKVL 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EXTRACELLULAR (POTENTIAL).
C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q9MZ41-1; Sequence=Displayed;
Name=2; Synonyms=CD94-B;
IsoId=Q9MZ41-2; Sequence=VSP_003056;
TISSUE SPENITIY: Natural killer cells.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7244D99E8D9587E7 CRC64;
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                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Type II membrane protein.
-!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                          Event=Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.0%; Score 155; DB 1; 27.0%; Pred. No. 3.2e-08; iive 28; Mismatches 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (S or send an email to license@isb-sib.ch).
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/FTId=VSP (
                                                                                                                      Immunol. 168:240-252(2002).
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                                                                                                                                                                                                                                                                                                                                                                                     Name=1; Synonyms=CD94-A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 27.0
Matches 47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179
176
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132
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163 AA.

PRT;

STANDARD;

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Eutheria; Primates; Catarrhini; Hominidae; Homo.
                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
DISULFID
                                                                                                                                                               complex."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         95 HCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDID---GW 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   58 NCYFFSEEKNNKSLAVERCKDMDGHLTSISSKEEFKFILRYKGPGNHWIGIEKVDFNGTW 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -----CKEGWVGYNK 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLE2_HUMAN STANDARD; PRT; 149 AA.
092478; 098478; 0984781;
28-FEB-2003 (Rel. 41, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
C-type lectin superfamily member 2 (Activation-induced C-type lectin).
CLECSF2 OR AICL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33 PCVSYLVMVALGLLTVILMS-----LLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGS
                                                                                                                                                                                                                                                                                                                                                                                                      Tomley F., Binns M., Campbell J., Boursnell M.E.G.,
"Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                 Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                           MEDLINE=20193820; PubMed=10729156;
Afonso C.L., Tulhan B.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"The genome of fowlpox virus.";
J. Virol. 74:3815-3831(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               142 RWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  of fowlpox virus.";
J. Gen. Virol. 69:1025-1040(1988).
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163 AA; 18635 MW; 5156DC8928855532 CRC64;
    16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Putative C-type lectin protein FPV239 (BamHI-ORF8)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.9%; Score 154; DB 1; 22.9%; Pred. No. 3.7e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMEL, D00295, BAA00203.1, -.
PIR, H29963, WMVZP8.
HSSP, P05140, 2AFP.
FIGHTERPEC, IPR001304, Lectin.C.
Pfam; PR00059; lectin.C; 1.
SMART; SM00034; CLECTY.
FACSITE; P800615; C. TYPE LECTIN.1; FALSE_NEG.
PROSITE; P850041; C.TYPE_LECTIN.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18 PCGS--IIIVLSVFVIILSTRPPVPPDIKILY---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C-TYPE LECTIN
                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=88229622; PubMed=2836548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AF198100; AAF44583.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Lectin.
                                                                                                                                                                                                                                                                                                                                                                 STRAIN=FP-9 / Isolate HP-438;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-116 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                         SECUENCE FROM N.A.
                                                                                                                                                             NCBI_TaxID=10261;
                                                                                          Fowlpox virus
                                                                                                                                          Avipoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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YESUBENCE KNOW N.A.

XX STUBLINE-22388257; PubbMed=12477932;
XX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
XX Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
XX Strausberg R.L., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
XX Altschul S.F., Zeeberg B., Buctow K.H., Schaefer C.F., Bhat N.K.,
XX Altschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heisch F.,
XX Brachento M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
XX Stapleton M., J. Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
XX Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gumaratne P.H.,
XX Norley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
XX Ilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
XX Helton E., Ketteman M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
XX Miting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
XX Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
XX Schiquez A.C., Grimwood J., Schmutz J., Myers R.M.,
XX Schein J.E., Jones S.J.M., Marra M.A.;
XX Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@ib.sib.ch).
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GO; GO:0005887; C:integral to plasma membrane; TAS.
GO; GO:0005530; F:lectin; TAS.
GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.
                                                                                                                                                                                                                                                                                                                                             Yokoyama-Kobayashi M., Yamaguchi T., Sekine S., Kato S., "Selection of cDNAs encoding putative type II membrane proteins on the cell surface from a human full-length cDNA bank.";
Gene 228:161-167(1999).
                                                                      Hamann J., Montgomery K.T., Lau S., Kucherlapati R., van Lier R.A.W., "AICL, a new activation induced antigen encoded by the human NK gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and mouse CDNA sequences.";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

-: SUBCELLULAR LOCATION: Type II membrane protein (Probable).

-: TISSUB SPECIFICITY: Expressed preferentially in lymphoid tissues, and in most hematopoietic cell types.

-: SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FOTENTIAL).
EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
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Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS00515; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
Glycoprotein; Transmembrane; Lectin; Signal-anchor.
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=99173880; PubMed=10072769;
SEQUENCE FROM N.A. MEDLINE=97190245; PubMed=9038101;
                                                                                                                                                                                                   [mmunogenetics 45:295-300(1997).
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63
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                                                                                                                                                                                                                                                                                                                              SMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG--WRWEDGP 147
                                                                                                                                                                                                                                                                                                                                                                  50 SKEEGDWNSSKYNCSTQHADLTIIDNIEEMNFLRRYKCSSDHWIGLKMAKNRTGQWVDGA 109
                                                                                                                                                                                                                                                                                            49
                                                                                                                                                                                                                                                                            Wang R., Kini R.M., Chung M.C.M.,
"Rhodocetin, a novel platelet aggregation inhibitor from the venom of
Calloselasma rhodostoma (Malayan pit viper): synergistic and
noncovalent interaction between its subunits.";
Biochemistry 38:7584-7593 (1999).
                                                                                                                                                                                                                                                    31 HRPCVSYL-VMVALGLLTVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- MASS SPECTROMETRY: MW=15955.90; MW ERR=1.44; METHOD=Electrospray.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
HSSP; P23806; 11XX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agkistrodon rhodostoma (Malayan pit viper) (Calloselasma rhodostoma)
Bukaryota, Matazoa, Chordate; Craniata, Vertebrata; Buteleostomi,
Lepidosauria, Squamata, Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Calloselasma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          together by noncovalent interactions rather than by intersubunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: A potent inhibitor of collagen-induced platelet aggregation. Individually, neither subunit inhibits platelet aggregation. Both subunits are essential. SUBUNIT: Heterodimer of one alpha and one beta subunit held
                                          (POTENTIAL).
                                                                                                                                                                                                              21;
                                                                            .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19;
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                                                                                                                                                                          14.8%; Score 153.5; DB 1; Length 149; 27.0%; Pred. No. 3.7e-08;
                                                                                                                                                                                                                Indels
                                                                                                                                    0B4FED23424F6C55 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                          148 ALSLSI-LSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
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BY SIMILARITY.
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N-LINKED (GLCNAC.
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M-S T (IN REF. 3).
D -> H (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, FUNCTION, SUBUNIT, AND MASS SPECTROMETRY.
                                                                                                                                                                                                                68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C-TYPE LECTIN (LONG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
18-FBB-2003 (Rel. 41, Last annotation update)
Rhodocetin alpha subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00059; lectin c; 1.
SMART; SM0034; CLECT; 1.
PROSITE; PS00615; C TYPE_LECTIN 1; FALSE_NEG-PROSITE; PS50041; C_TYPE_LECTIN 2; 1.
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BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=99303998; PubMed=10360956;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro, IPR001304; Lectin C.
                                                                                                                                      17307 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15962 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40; Conservative
                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
  144
136
57
62
100
79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     102
133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                    149 AA;
                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Viperidae, Crota
NCBI_TaxID=8717;
  87
123
57
62
100
79
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                                                                                                                                                                                                                43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RHCA AGKRH
P81397;
DISULFID
DISULFID
CARBOHYD
                                                                                            CONFLICT
CONFLICT
SEQUENCE
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                                                          CARBOHYD
                                                                            CARBOHYD
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                                                                                                                  61 NKIYRSWIGLKIENKGORSNIEWSDGSSISYENLYEPYMEKCFLMDHOSGLPKWHTADCE 120
CPNLWMRNGSHCYYFSMEKRDWNSSLKFCA--DKGSHLLTFPDNQGVNLFQEYVGEDFY- 131
                          2 CPDGWSSIXSYCYRPFKEKKIWEEAERFCTEQEKEAHLVSM-ENRLEAVFVDMVMENNFE 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. Usage the or serial in no or send an email a license agreement.
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INTERCHAIN (WITH C-158 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (WITH C-104 IN ALPHA CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Crotalus durissus terrificus (South American rattlesnake).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Lepidosauria, Squamata, Scleroglossa, Serpentes, Colubroidea,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycoprotein VI (GPVI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leduc M., Bon C.;
"Cloning of subunits of convulxin, a collagen-like platelet-
"Cloning of subunits of corvalus durissus terrificus venom.";
Biochem. J. 333:389-333(1998).
-!- FUNCTION: Binds to the platelet and collagen receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 24-53; 99-109 AND 126-145.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 140.5; DB 1; Length 148; Pred. No. 7.1e-07;
                                                                                          ---WEDGPALSLSILSNSVVQKCGTI-HRCGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94D7E3E1BC693B9F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                             28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONVULXIN BETA.
                                                                                                                                                                                                                                                                                                                                                      148 AA
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PSO0615; C_TYPE_LECTIN_1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Convulxin beta precursor (CVX beta).
                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis ac.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Venom gland;
MEDLINE=98324901; PubMed=9657980;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viperidae; Crotalinae; Crotalus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam, PF00059, lectin c; 1.
PRINTS, PR01504; PNCREATITSAP.
SMART, SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MM;
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29.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Y16349; CAA76182.1; -.
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                                                                                          ---WIGLR-DIDGWR
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17402 I
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                                                                                                                                                                                                                                 121 EKNVFMCKFQLP 132
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148 AA;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=8732;
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Q9YGG9;
                                                                                                                                            СНВВ СКОНО
Р81509;
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                                                                                                       RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               94
                                      39 VMVALGLLIVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNS 98
                                                                                 50
                                                                                                                        SLKFCADK--GSHLLTFPDNQGVN----LFQEYVGEDFYWIGLRDI---DGWRWEDG 146
                                                                                                                                                  VSYLVMVALGLITVILMSLILYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomley F., Binns M., Campbell J., Boursnell M.E.G.; "Sequence analysis of an 11.2 kilobase, near-terminal, BamHI fragment
  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20193820; PubMed=10729156;
Afonso C.L., Tulman B.R., Lu Z., Zsak L., Kutish G.F., Rock D.L.;
"The genome of fowlpox virus.";
    23;
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                                                                                                                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Putative C-type lectin protein FPV008/FPV253 (BamHI-ORF2).
FPV008 AND FPV253.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13.2%; Score 137; DB 1; Length 16'
29.1%; Pred. No. 1.8e-06;
.ive 21; Mismatches 78; Indels
  39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Virol. 74:3815-3831(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMEN: B29963; WMVZF2.
InterPro; IPR001304; Lectin_C.
Pfam; PR00059; lectin_c; 1.
PR081T; S000034; CLECT; 1.
PROSITE; PS00615; C_TYPE_LECTIN_1; FALSE_NEG.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                       167 AA.
  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C-TYPE LECTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gen. Virol. 69:1025-1040(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=88229622; PubMed=2836548;
  21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF198100; AAF44607.1; -.
                                                                                                                                                                                                                                                                                                           01-JAN-1990 (Rel. 13, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=FP-9 / Isolate HP-438;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hypothetical protein; Lectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; D00295; BAA00192.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               44; Conservative
  Conservative
                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             fowlpox virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10261;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Avipoxvirus
34;
                                                                                                                                                                                                                                                                    V008 FOWPV
P14370;
                                                                               S
                                                                                                                          66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                 VOOR FOWPV
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  Matches
                                                                                                                                                                                                                              RESULT
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75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADK--GSHLLITFPDNQGVNLFQEYVGEDFYW 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 CPSDWSSYEGHCYRVFQQEMTWDDAEKFCTQQHTGGHLVSFRSSEEVDFLVSILKFDLFW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (WITH C-81 IN ALPHA CHAIN) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last annocation update)
Mamushigin alpha chain precursor.
Agkistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                             Bukaryota, Metazoa; Chordata, Craniata; Vertebrata, Buteleostc
Lepidosauria, Squamata, Scleroglossa, Serpentes; Colubroidea;
Viperidae, Crotalinae; Crotalus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07835BBCB61E9EAD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                               Crotalus horridus horridus (Timber rattlesnake).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.4e-06;
                                                                                                                                                             (Rel. 41, Last sequence update)
(Rel. 41, Last annotation update)
                                124 EQGVNDICLLFDTSNIIEMSCIFHERTICVK 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     157 AA.
                                                                                                                  117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-TYPE LECTIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.8%; Score 132.5;
155 SNSVVQKCGTIHRCGLHASSCEVALQWICEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PEAM, PRO0059, lectin c; 1. PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CLECT; 1. PR0051TE; PS00615; C TYPE LECTIN 1; 1. PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                               TISSUE=Venom;
MEDLINE=96420502; PubMed=8823201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     133 IGLRDIDGW-----RWEDG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          : | | | | : | | | | MGWRDI--WNERRLQWSDG 78
                                                                                                                                                 28-FEB-2003 (Rel. 41, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13888 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      31.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116
13
115
92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     95 1
117 AA;
                                                                                                                                                                                               CHH-B beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93229
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DISULFID
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHAIN
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                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99 SLKFCADK--GSHLLTFPDNQGVNLFQEYVGE-----DFYWIGL-----RDIDGWRWEDG 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5 IFVSFGLL-VVFLSL-----SGAE-----DDSDCPSDWSSNGRFCYKLFQQKMKWAD 50
                                                    TISSUE-Venom:

MEDLINE-98319530; PubMed=9657448;

MEDLINE-98319530; PubMed=9657448;

Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M.,

Suzuki M., Matsui T., Titani K., Yoshioka A.;

"The CDNA cloning and molecular characterization of a snake venom
platelet glycoprotein Ib-binding protein, mamushigin, from Agkistrodon
halys bromhoffii venom.";

Thromb. Haemost. 79:1199-1207(1998).

-! FONCTION: Binds to platelet glycoprotein Ib and enhances platelet
aggregation at low-shear stress. At high-shear stress, aggregation
is inhibited.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39 VMVALGLLIVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNS
                                          SEQUENCE FROM N.A., SEQUENCE OF 22-58, SUBUNIT, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C-98 IN BETA CHAIN)
                                                                                                                                                                                                       SUBCELLULAR LOCATION: Secreted.
MASS SPECTROMETRY: NW=16825; NW_ERR=2.7; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26;
 Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                   SUBUNIT: Heterodimer of alpha and beta chains; disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY).
BY SIMILARITY.
47DAA17891CE1865 CRC64;
                                                                                                                                                                                                                                             SIMILARITY: Contains 1 C-type lectin family domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAMUSHIGIN ALPHA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 131; DB 1;
Pred. No. 6.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INTERCHAIN (WITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-TYPE LECTIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005576; C:extracellular; IC.
GO; GO:0007596; P:blood coagulation; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C TYPE_LECTIN_2; 1.
Blood coagulation; Lectin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR001304; Lectin C.
InterPro; IPR003990; Pancreatis ac.
Lepidosauria; Squamata; Sclerog
Viperidae; Crotalinae; Gloydius
                                                                                                                                                                                                                                                                                                                                                             EMBL; AB019615; BAA34424.1; -.
HSSP; P23806; 1IXX.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS; PR01504; PNCREATITSAP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSVSYENLVKPNSKKC 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18333 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  147 PALSISISNSVVOKC 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.6%;
27.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00059; lectin c; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 37; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21
152
152
38
151
103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  157 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
          Viperidae, Crotali
NCBI_TaxID=242054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22
34
27
55
103
                                                                                                                                                                                                linked
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DISULFID
DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
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146 AA.

PRT;

STANDARD;

RESULT 11 MMHB AGKHA ID MMHB AGKHA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7;
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                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=98319530; PubMed=9657448; Sakurai Y., Fujimura Y., Kokubo T., Imamura K., Kawasaki T., Handa M., Suzuki M., Matsui T., Titani K., Yoshioka A.; The cDNA cloning and molecular characterization of a snake venom platelet glycoprotein ib-binding protein, mamushigin, from Agkistrodon halys bromhoffii venom."; Thromb. Haemost. 79:1199-1207(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: Binds to platelet glycoprotein Ib and enhances platelet aggregation at low-shear stress. At high-shear stress, aggregation
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., SEQUENCE OF 24-56, SUBUNIT, AND MASS SPECTROMETRY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39 VMVALGLLTVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 IFLSFGLLVVFVS------LSGTGADCPSDWSSYEGHCYRVFOKEMTWED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INTERCHAIN (WITH C-103 IN ALPHA CHAIN)
10-0cT-2003 (Rel. 42, Last sequence update)
10-0cT-2003 (Rel. 42, Last sequence update)
10-0cT-2003 (Rel. 42, Last annotation update)
Mamushigin beta chain precursor.
Mamushigin beta chain precursor.
Makistrodon halys blomhoffi (Mamushi) (Gloydius blomhoffii).
Eukaryota, Metazoa; Chordeta; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- SUBCELLULAR LOCATION: Secreted.
-!- MASS SPECTROMETRY: MW=15413; MW_ERR=6; METHOD=Electrospray;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: Heterodimer of alpha and beta chains; disulfide-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                52; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9EDA84BDCC24E76D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                148 ALSLSILSNSVVQKCGTIHRCGLHASSCEVAL----QWI 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --HNAWITEŚECIAAKTTDNOWL 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.5%; Score 130; DB 1; 24.5%; Pred. No. 7.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MAMUSHIGIN BETA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (BY SIMILARITY)
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C-TYPE LECTIN.
BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00615; C TYPE LECTIN 1; 1. PROSITE; PS50041; C TYPE LECTIN 2; 1. Blood coagulation; Lectin; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GO; GO:0005576; C:extracellular; IC. GO; GO:0007596; P:blood coagulation; InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                  Viperidae; Crotalinae; Gloydius
NCBI_TaxID=242054;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB019616; BAA34425.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23
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146 AA;
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Matches 39; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RANGE=24-146.
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TISSUE=Venom
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@ib.eib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsuzaki R., Yoshihara B., Yamada M., Shima K., Atoda H., Morita T., "cDNA cloning of IX/X-BP, a heterogeneous two-chain anticoagulant protein from snake venom.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COAGULATION FACTOR IX/FACTOR X-BINDING PROTEIN B CHAIN.
C-TYDE LECTIN (LONG FORM).
BY SIMILARITY.
                                                                                                                                                                               Trimeresurus flavoviridis (Habu).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
Viperidae; Crotalinae; Trimeresurus.
                                                                     IXB_TRIFL STANDARD; PRT; 146 AA.
P23807; Q91247;
D1-NOV-1991 (Rel. 20, Created)
15-UUL-1998 (Rel. 36, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Coagulation factor IX/factor X-binding protein B chain precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Atoda H., Hyuga M., Morita T.; "The primary structure of coagulation factor IX/factor X-binding protein isolated from the venom of Trimeresurus flavoviridis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homology with asialoglycoprotein receptors, proteoglycan core protein, tetranectin, and lymphocyte Fc epsilon receptor for immunoglobulin B.";
                                                                                                                                                                                                                                                                                                                                                                                               Biochem. Biophys. Res. Commun. 220:382-387(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00034; CLECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; CTYPE_LECTIN_2; 1.
Lectin; Calcium; Signal; 3D-structure.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 266:14903-14911(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PDB; 11XX; 06-MAY-98.

PDB; 1BJ3; 16-AUG-99.

INTERPRO; 1PR001304; Lectin C.

INTERPRO; 1PR003990; Pancreātis_ac.

PÉMN; PF00059; lectin c; 1.

PRINTS; PR01504; PNCRĒATITSAP.
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=96184662; PubMed=8645314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91332000; PubMed=1831197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D83332; BAA11888.1; -. PIR; JC4691; JC4691.
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36
                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 24-146.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Venom;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
DISULFID
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                                       RESULT 12
                                                                                         A PARTER AND DEPARTMENT OF COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COLOR COL
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99 SLKFCADK--GSHLLTFFDNQGVNL----FQEYVGEDFYWIGLRDI---DGWRWEDGPA 148
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---LSGTAADCPSDWSSYEGHCYKPFSEPKNWAD 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T., Fukui H., Sugimoto M., Ruggeri Z.M.;
"Isolation and chemical characterization of two structurally and functionally distinct forms of botrocetin, the platelet coagglutinin Biochemistry 30:1957-1964(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               43; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIJNE 93157385; PubMed=8430107; Usami Y., Fukimara Y., Suzuki M., Ozeki Y., Nishio K., Fukui H., Titani K.; "Primary Structure of two-chain botrocetin, a von Willebrand factor modulator purified from the venom of Bothrops jararaca."; Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bothrops jararaca (Jararaca).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                 INTERCHAIN (WITH C-102 IN A CHAIN) BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 LRYKAWAEESYCVYFKSTNNK------WRSRACRMAQFVCE 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L-----SLSILSNSVVQKCGTIHRCGLHASSCEVALQWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16922 MW; 8E1961C59F96757C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-AUG-1991 (Rel. 19, Created)
01-UUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Botrocetin, alpha chain (Platelet coagglutinin).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12.3%; Score 127.5; DB 1
20.7%; Pred. No. 1.3e-05;
ive 28; Mismatches 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                133 AA
BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Venom;
MEDLINE=91129280; PubMed=1993206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viperidae, Crotalinae, Bothrops.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, AND DISULFIDE BONDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 20.74
Matches 34, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5 IFMSFGFLVVFLS--
  146 AA;
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SUBUNIT: Heterotetramer of the subunits 1,
                                                                                                                                                                                                                                                                                                               121
13
119
                                    disulfide-linked.
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2
30
30
123 AA;
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Local S...
27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BOTB BOTJA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ritani K.;
                                                                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                        DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                 DISULPID
                                                                                                                                                                                                                                                                                          Lectin.
DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BOTB_BOTJA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | : | | : | : | : | : | | : | | : | | CPSGMSSYEGNCYKFFQQKMNWADAERFCSEQAKGGHLVS-----IKIYSKEKDFVGDL 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            platelets.";
Thromb. Haemost. 79:609-613(1998).
-!- FUNCTION: Binds to platelet GPIb/IX receptor system and stimulates
agglutination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCAD--KGSHLLIFPDNQGVNLF---QEYVGE-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                      platelet agglutination.
FUNCTION: There are two distinct forms of the von Willebrand factor-dependent platelet coagglutinin. The dimeric form is 34-times more active than the one-chain botrocetin in promoting vWF binding to platelets.
SUBUNIT: Disulfide-linked dimer of an alpha and a beta chain. Botrocetin and vWF form a soluble complex.
SUBCELLULAR LOCATION: Secreted.
SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                               toxin botrocetin.";
Structure 10:943-950(2002).
-!- FUNCTION: Two-chain botrocetin forms an activated complex with vWF, and the complex then binds to platelet GPIb, resulting in
                                                                                                          "Structural basis of von Willebrand factor activation by the snake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INTERCHAIN (WITH C-75 IN BETA CHAIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --DFY-WIGLRDID-----GWRWEDGPALSLSILSNSVVQKCGTIHR 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Alboaggregin A subunit 4.
Trimeresurus albolabris (White-lipped pit viper).
Rekaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                      MEDLINE=22118144; PubMed=12121649;
Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
Liddington R.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIJNE-98189535; Pubmed-9531050;
Kowalska M.A., Tan L., Holt J.C., Peng M., Karczewski J.,
Calvete J.J., Niewiarowski S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15215 MW; E4CF4502946AC74B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; Score 126; DB 1;
; Pred. No. 1.7e-05;
24; Mismatches 33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            123 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12.2%; Score 126;
                CRYSTALLOGRAPHY (2.6 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00615; C TYPE LECTIN 1; PROSITE; PS50041; C TYPE LECTIN 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A47267; A47267.
PDB; 1LJK; 17-JUL-02.
PDB; 1FWU; 14-FBB-01.
InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00356; ANTIFREEZEII.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128
80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00034; CLECT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lectin; 3D-structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          133 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
les 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=8765;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABA4 TRIAB
P81114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             129
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CPNLWMRNGSHCYYFSMEKRDWNSSLKFCAD--KGSHLLTFPDNQG----VNLFQEYVGE 128
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujimura Y., Titani K., Usami Y., Suzuki M., Oyama R., Matsui T., Fukui H., Sugimoto M., Ruggeri Z.M.;
"Isolation and chemical characterization of two structurally and thuctionally distinct forms of botrocetin, the platelet coagglutinin isolated from the venom of Bothrops jararaca.";
Biochemistry 30:1957-1964(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Primary structure of two-chain botrocetin, a von Willebrand factor modulator purified from the venom of Bothrops jararaca.";
Proc. Natl. Acad. Sci. U.S.A. 90:928-932(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Structure 10:943-950(2002).
-!- FUNCTION: Two-chain botrocetin forms an activated complex with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'Structural basis of von Willebrand factor activation by the snake
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-AUG-1991 (Rel. 19, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Botrocetin, beta chain (Platelet coagglutinin).
Bothrops jararaca (Jararaca).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jsami Y., Fujimura Y., Suzuki M., Ozeki Y., Nishio K., Fukui H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fukuda K., Doggett T.A., Bankston L.A., Cruz M.A., Diacovo T.G.,
Liddington R.C.;
                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 123;
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2, 3 and
                                                                                                                                                                                                                                                              C-TYPE LECTIN (LONG FORM).
BY SIMILARITY.
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BY SIMILARITY.
A; D4CFBEE1219C9B1E CRC64;
                              -!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Contains 1 C-type lectin family domain.
                                                                                                                                                                                                                                                                                                                                                                                     12.0%; Score 124.5; DB 1;
31.4%; Pred. No. 2.2e-05;
tive 15; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         129 DFYWIGLRDIDGW-----RWEDGPAL 149
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MEDLINE=22118144; PubMed=12121649;
                                                                                                                                 Pfam; PP00059; lectin c; 1.
PRINTS; PR00356; ANTIFREEZEII.
SMART; SM00034; CIECT; 1.
PROSITE; PS00615; C TYPE LECTIN 1; 1.
PROSITE; PS50041; C TYPE LECTIN 2; 1.
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                                                                     HSSP, P23807; IIXX.
InterPro; IPR002353; Antifreezell.
InterPro; IPR001304; Lectin_C.
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14365 MW;
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                         Gaps
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VWF, and the complex then binds to platelet GPIb, resulting in
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Search completed: August 10, 2004, 16:42:48 Job time : 9 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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using sw model OM protein - protein search, Run on:

August 10, 2004, 16:39:05; Search time 32 Seconds (without alignments) 1853.669 Million cell updates/sec

US-09-811-367B-5 Perfect score:

1036 1 MADNSIYSTLELPAAPRVQD......GLHASSCEVALQWICEKVLP 188 Sequence:

BLOSUM62 Scoring table:

1017041 seqs, 315518202 residues Gapop 10.0 , Gapext 0.5 Searched:

396094 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 188

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

sp_archea:* sp_bacteria:* SPTREMBL 25:* Database

sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:*
sp_phage:*
sp_plant:*
sp_plant:*
sp_rodent:* sp_vertebrate:*
sp_unclassified:* sp_rvirus:*
sp_bacteriap:* 111. 123. 144. 115. 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

088713 mus musculu Q9nzsl homo sapien O54708 mus musculu O54707 mus musculu Q9r007 mus musculu 0991f4 sus scrofa 08b124 mus musculu 0951g4 bos taurus 0991f3 sus scrofa 09mhy8 pongo pygma 08wup7 homo sapien Q8spx0 sus scrófa Q9ny25 homo sapien Q8mji3 pongo pygma O35778 rattus norv Q64335 rattus norv O88713 mus musculu Description SUMMARIES Q64335 O88713 Q9NZS1 O54708 O54707 Q9R007 Q9NY25 Q8MJI3 Q35778 Q8BL24 Q95JG4 Q9GLF3 Q8MHY8 Q8WUP7 Q9GLF4 **OSSPX**0 а 11 Query Match Length DB 179 179 165 165 100.0 178 175 175 173 171 165.5 161.5 160 160 159.5 158.5 158.5 Score 489788788484 Result Ņ.

Ognzj6 macaca mula Ogr4k5 rattus norv Ogd188 rat cytomeg Ogd188 rat cytomeg Ogd189 mus musculu Ogukg0 homo sapien Ogni44 pongo pygma Ogly44 agkistrodon Ogjkf2 mus musculu Ogly67 homo sapien Ogliw1 agkistrodon Ogjiw1 agkistrodon Ogjiw1 agkistrodon Ogjiw1 agkistrodon Ogjiw1 agkistrodon Ogjiw1 agkistrodon Ogjiw1 agkistrodon Ogjiw1 agkistrodon Ogjiw1 agkistrodon Ogjiw2 homo sapien Ogjw2 hom sapien Ogjw2 hom sapien Ogjw2 hom sapien Ogjw2 hom usculu Ogjw2 mus musculu Ogjk5 mus musculu Ogjk5 mus musculu Ogjk5 mus musculu Ogjk5 mus musculu Ogjk5 mus musculu Ogjk5 mus musculu Ogjk9 macaca mula Ogjk9 macaca mula Ogjk9 macaca mula Ogjk6 macaca mula Ogjk9 macaca mula Ogjk9 macaca mula Ogjk9 macaca mula Ogjk9 macaca mula Ogjk9 macaca mula Ogjk9 macaca mula	
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1111 122222222222222222222222222222222	4 4 4 4 C C 4 C

ALIGNMENTS

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MEDLINE=96016176; PubMed=7568140;

Guthmann M.D., Tal M., Pecht I.;

Guthmann M.D., Tal M., Pecht I.;

Guthmann M.D., Tal M., Pecht I.;

A secretion inhibitory signal transduction molecule on mast cells is another C-type lectin.",

Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).

EMBL, X97192; CAA65829.1; JOINED.

EMBL, X97193; CAA65829.1; JOINED.

EMBL, X97194; CAA65829.1; JOINED.

EMBL, X97195; CAA65829.1; JOINED.

EMBL, X97195; CAA65829.1; JOINED.

EMBL, X97195; CAA65829.1; JOINED.

EMBL, X97195; CAA65829.1; JOINED.

EMBL, X97195; CAA65829.1; JOINED.

EMBL, X97195; CAA65829.1; JOINED.
                                                                                                                               Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                           PIR, 159421; 159421.

GO; GO: 0005529; F: sugar binding; IEA.

InterPro; IPRO134; Lectin C.

Pfam; PF00059; lectin c; 1.

SMART; SM00034; CLECT; 1.

PROSITE; PSS0041; C_TYPE LECTIN 2; 1.

PROSITE; PSS0041; C_TYPE LECTIN 2; 1.
                                                                       Last sequence update)
Last annotation update)
                               188 AA.
                                                           Created)
                             PRT;
                                          Q64335;
01-NOV-1996 (TrEMBLrel. 01,
01-NOV-1996 (TrEMBLrel. 01,
01-OCT-2003 (TrEMBLrel. 25,
                             PRELIMINARY;
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                                                                                                     MAFA protein.
                             064335
RESULT 1
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120

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101 IIHDQLEMAFIQKNLRQLNYVWIGLNFTSLKMTWTWVDGSPIDSKIFFIKGPAKENS--- 157
                                                                                                                                               61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTPPDNQGVK 120
                                                                                                                                                                                                            LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180
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                                              1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                    CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFFDNQGVN
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                           1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
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Bur. J. Immunol. 30:568-576(2000).

EMBL, AF175207; AAF37805.1; -..
GO; GO:0016020; c:membrane; TAS.

InterPro; IPR001304; Lectin_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20135860; PubMed=10671213;
Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
Fernandez-Ruiz E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UJN-2003 (TrEMBLrel. 24, Last annotation update)
Lectin-like receptor F1, splice variant 1 KLRF1-s1.
KLRF1.
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6.2e-11;
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25.0%; Pred. No. 6.2e
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181 WICKKVL 187
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Matches
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054708
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MEDLINE=99077194; PubMed=9862378;
Hanke T., Corral L., Vance R.E., Raulet D.H.;
"2F1 antigen, the mouse homolog of the rat '$1', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
Eur. J. Immunol. 28:4409-4417(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=129/SvevTACfBr; TISSUE=Spleen;
MEDLINE=21115136; PubMed=11220622;
Voehringer D., Kaufmann M., Pircher H.;
"Genomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor G1 gene (KLRG1), the mouse homologue
                                                                                                                                     MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                           CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN
                                                                                                                                                                                                                                                                                                                  LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ
                                                                                                                                                                                                                                                                                      LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ
                                                                                                1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ol-AUG-1999 (TrEMBLrel. 11, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last amotation update)
Mast cell function-associated antigen 2F1 (MAFA) (Killer cell lectin-
like receptor G1).
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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    11; Length 188;
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                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Blaser C.;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21396 MW; 876336802EA134F1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell adhesion; IEA
                                                 0
  100.0%; Score 1036; DB 1.
100.0%; Pred. No. 1e-102;
iive 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     188 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1355294; KIRGI.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenetics 52:206-211(2001).
EMBL, AP097357, AAD03718.1; -.
EMBL, AJ010751; CAA09342.1; -.
EMBL, AF317727; AAK40082.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1998 (TrEMBLrel. 08, 01-AUG-1999 (TrEMBLrel. 11, 01-OCT-2003 (TrEMBLrel. 25,
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SEQUENCE OF 2-188 FROM N.A.
Query Match 100.
Best Local Similarity 100.
Matches 188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                  WICEKVLP 188
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Type II transmembrane protein MDL-1 (C-type).
CLECSF5 OR MDL1.
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EMBL; AK036697; BAC29537.1; -.
MGD; MGI.145151; Clecsf5.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0005529; F:sugar binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               165 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36; Mismatches
    STRAIN=C57BL/6J; TISSUE=Mammary gland;
                                                                                                                                                                                                                                                                                                                       PROSITE; PS50041; C_TYPE_LECTIN_2; 1. PROSITE; PS00022; EGF_1; 1.
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01-MAY-2000 (TrEMBLrel. 13, Last seq
01-OCT-2003 (TrEMBLrel. 25, Last ann
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STRAIN-ECSTBL/60, TISSUE-Bone,
MEDIINE-22354683; PubMed=12466851;
The FANTOM CONSORTIUM,
                                                                                                        EMBL; AF030311; AAC28243.1; -. EMBL; AF057714; AAC33713.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          60,770 full-length cDNAs.";
Nature 420:563-573(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50; Conservative
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22 SRWKVKAVLHR-PCVSYLVMVALGLLTVILMSLLLYQRTLC-CGSKGFM-CSQCSRCPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                             MEDLINE=98124458; PubMed=9464811;
Vance R.B., Tanamachi D.M., Hanke T., Raulet D.H.;
"Cloning of a mouse homolog of CD94 extends the family of C-type
lectins on murine natural killer cells.";
Eur. J. Immunol. 27:3236-3241(1997).
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Heusel J.W., Ho E.L., Brown M.G., Matsumoto K., Yokoyama W.M.;
"Murine CD94.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Killer cell lectin-like receptor, subfamily D, member 1 (CD94).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.9%; Score 175; DB 11; Length 179; 27.9%; Pred. No. 1.3e-10; ive 36; Mismatches 71; Indels 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20809 MW; D59E1CBB63139E45 CRC64;
                                                                Last sequence update)
Last annotation update)
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Vance R.E., Tanamachi D.M., Hanke T., Raulet D.H.;
Bur. J. Immunol. 27:0-0(1997).
  179 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:1196275; KIrdi.
GO; GO:005529; F:sugar binding; IEA.
InterPro; IPR006209; EGF like.
InterPro; IPR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
PROSITE; PS50041; CIYPE LECTIN_Z; 1.
PROSITE; PS00022; EGF_1; 1.
                                          Created)
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PRT;
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                 O54708;
01-JUN-1998 (TrEMBLrel. 06,
01-JUN-1998 (TrEMBLrel. 06,
01-OCT-2003 (TrEMBLrel. 25,
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PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 AA;
                                                                                                                                                                                                                                                                         STRAIN=CB.17 SCID;
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                                                                                                                                                                                                          NCBI_TaxID=10090;
                                                                                                                            KLRD1 OR CD94.
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79 WMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL--- 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123 EKRNAWLWEDGIVPSKDLFPEFSVIRP----EHCIVYSPSKSVSAESCENKORYICKKL 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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STRATE-BALB-C; TISSUE-Myeloid;
MEDLINE-99380598; PubMed=10449773;
Bakker A.B., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.;
"Myeloid DAP12-associating lectin (MDL)-1 is a cell surface receptor involved in the activation of myeloid cells.";
proc. Natl. Acad. Sci. U.S.A. 96:9792-9796(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
Butcher S., Cottage A., Cook G.P., "Mouse natural killer cell receptors homologous to human CD94 and NKG2-D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 179;
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                                                                                                     (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE 179 AA; 20808 MW; DD343419E93B3465 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                               EMBL; AF039025; AAD02116.1; -.
MGD; MG1:1196275; Klrd1.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
InterPro; IPR006209; EGF_like.
Pfam; PF00059; Lectin_C.
Pfam; PF00059; Lectin_C.
SMART; SM00034; CLECT; 1.
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Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  92 EKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG---WRWEDGPA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 SENSWINISMINFCKQKGSTLAIVNTPEKLKFLQNISGAEKYFIGLLYQPAEKMWRWINNSV 124
                                                                                                             82
                                                                                                                                 5 MIISGLIVVVIKVVGMTFFLLYFSQIFGRNDESTMPTRSYGTV-----CPRNWDFHQGK 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 MVALGLLTVIL-----MSLLLYQRTLCCGSKGFMCSQC--SRCPNLWMRNGSHCYYFSM 91
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                                                                                                                                                        86 CYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGLRDIDG---WR
                                                                                                            ----- QRTLCCGSKGFMCSQCSRCPNLWMRNGSH
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                                                                                       Gaps
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Yim D., Jie H.B., Sotiriadis J., Kim Y.S., Kim Y.B.;
"Molecular cloning and expression pattern of porcine myeloid DAP12-associating lectin-1.";
Cell. Immunol. 209:42-48 (2001).
EMBL; AP28549; AA629477.1;
GO; GO:0005229; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
InterPro; IPR001304; Lectin_C.
EMBR; PR00059; lectin_C.
SMART; SM00034; CLECT: 1.
                                                                                                                                                                                                                                                                                                                                      Myeloid DAP12-associating lectin short form.

Sus scrofa (Pig).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;

Mammalia; Butheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                       30;
                                                               ; Score 173; DB 11; Length 165;
; Pred. No. 1.9e-10;
28; Mismatches 61; Indels 3
                                                                                                                                                                                                    143 WEDGPALSISILSNSVVQXCGTIHRCGL----HASSCEVALQWICE 184
                                                                                                                                                                                                                 Length 165;
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                                          165 AA; 19055 MW; 626D64392A513282 CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                                                  165 AA
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     SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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28.3%;
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                                                                                      47; Conservative
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Best Local Similarity
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                               Transmembrane
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Q8BL24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58
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MEDLINE=22354683; PubMed=12466851;
The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
"Analysis of the mouse transcriptome based on functional annotation of 7.70 full-length CDNAs.";

MAINTE 420:563-573 (2002).

EMBL; AK046600; BAC32802.1; -..
GO; GO:0005529; F:sugar binding; IEA.
InterPro; IPR001304; Lectin.C.
Frank; PR00059; lectin.C.
SMART; SM00034; CLECT; 1.
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinne; Bos.
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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"Homologues of natural killer cell receptors NKG2-D and NKR-P1
expressed in catile.",
Vet. Immunol. Immunopathol. 80:339-344(2001).
BMB1, AF322886; AK73811.1,
GO, GO:0004872; F:receptor activity; IEA.
GO, GO:000559; F:sugar binding; IEA.
InterPro; IFR001304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
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01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Natural killer cell receptor protein 1 variant 1 (Fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      59; Indels
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SEQUENCE 164 AA; 18927 MW; DF0AE012C049CIC0 CRC64;
Created)
Last sequence update)
Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19, Last seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Spleen;
MEDLINE=21351526; Pubmed=11457486;
(TrEMBLrel. 23, TrEMBLrel. 23, TrEMBLrel. 25,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            48; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                          C-type.
Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10090;
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                                                 01-MAR-2003
01-OCT-2003
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79 WMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL--- 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-22072192; PubMed=12077248; Guethlein L.A., Flodin L.R., Adams E.J., Parham P.; Apivotal Wink Cell Receptors of the Orangutan (Pongo pygmaeus): A Pivotal Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       24 WKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCG----SKGFMCSQCSRCPNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 RDIDGWRWEDGPALS---LSILSNSVVQKCGTIHRCG-LHASSCEVALQWICEKVL 187
                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
NCBI TaxID=9600;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     179 AA; 20550 MW; 6752CB8F182CFD73 CRC64;
                                 01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Natural killer cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TYEMBLrel. 20, Created)
01-MAR-2002 (TYEMBLrel. 20, Last sequence update)
01-OCT-2003 (TYEMBLrel. 25, Last annotation update)
Similar to lectin-like NK cell receptor.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL, BC019883, ARH19883.11.

GO, GO:0004872; F:receptor activity; IEA.

GO, GO:0005529; F:sugar binding; IEA.

GO, GO:000157; P:heterophilic cell adhesion; IEA.

Interpro, IPR001304; Lectin_C.

Pfam; PR00059; lectin_G:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.6%; Score 161.5; DB 6; Best Local Similarity 27.3%; Pred. No. 3.6e-09; Matches 48; Conservative 25; Mismatches 84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Immunol. 169:220-229(2002).

BMBL; AP470381; AAM78481.1;

EMBL; AP470382; AAM78482.1;

GO; GO:0004872; F:receptor activity; IEX

GO; GO:0005529; F:receptor activity; IEX

INTERPRO; IPR006209; EGF like.

INTERPRO; IPR001304; Lectin...

PFAM; PR00134; CLECT...

PROSITE; PS50041; C.TYPE LECTIN.2; 1.

PROSITE; PS50041; C.TYPE LECTIN.2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                  Pongo pygmaeus (Orangutan)
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                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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TISSUE=Testis;
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NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   with MHC-C
                                                                                                                                                      POPY-CD94.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Receptor.
SEQUENCE
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                                                                                                                                                                                                        75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLITFPDNQGVNLFQEYVGED--FYW 132
                                                                                                                                                                                                                                                   IGLR-DIDG--WRWEDGPALS---LSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKV 186
                                                                                                                                                                                                                                                                                                                                                                                 101 IGINFTLSGKSWKWINGSFLNSNILPIFGDAKEDCCVYISKTQCISDYCAAKNRWICQKE 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFY 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 WIGLRDIDG---WRWEDGPALSLSILSNSVVQKCGTIHRCGL----HASSCEVALQWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               :||| :||:| :||| 1135 FIGLLYQPAEKMMRWINNSVFNGSVISHSHNFNCVTI---GLTKTFDAASCDVNYRSICE 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         74
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21308528; PubMed=11414735;
Yim D., Jie H.B., Sotiriadis J., Kim Y.S., Kim Y.B.;
"Molecular cloning and expression pattern of porcine myeloid DAP12-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sus scrofa (Pig).

Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae, Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           38;
                                                                                            Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 6; Length 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match 15.8%; Score 164; DB 6; Length 18 Best Local Similarity 27.1%; Pred. No. 2e-09; Matches 49; Conservative 22; Mismatches 72; Indels
   161
18648 MW; 24F9AA44A19EAFB7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20835 MW; DA6ECOAF58BC95CE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell. Immunol. 209:42-48 (2001).

EMBL; AF284450; AAG29428.1; -.

EMBL; AF284450; AAG29428.1; -.

GO; GO:0005529; F:sugar binding; IEA.

GO; GO:0007157; P:heterophilic cell adhesion; IEA.

InterPro; IPR001304; Lectin_C.

SMART; SM00034; CLECT; 1.

PROSITE: PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40 MVALGLIVIL----MSLLLYQRTLCCGSKGFMCSQCSR-
                                                                                   Match 15.9%; Score 165; DB 6; Local Similarity 31.4%; Pred. No. 1.3e-09; les 38; Conservative 19; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 AA.
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01-MAR-2001 (TrEMBLrel. 16, Last sequence u
01-OCT-2003 (TrEMBLrel. 25, Last annotation
Myeloid DAPI2-associating lectin long form.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        associating lectin-1
161
161 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      185 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           187 L 187
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NON TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                            133
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                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9GLF3;
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Q8MHY8
ID Q8MHY
                                                                                                                                                Matches
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179 AA
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EMBL, AF470384; AAM78484.1; -.

GO; GO:0004872; F:receptor activity; IEA.

GO; GO:0005529; F:sugar binding; IEA.

InterPro; IPR005209; EGF like.
                                                                                                                                                                                                                                                        PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Natural killer cell receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pongo pygmaeus (Orangutan).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00059; lectin c; 1. smarr; smoo034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                   47; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
         SEQUENCE FROM N.A.
Mueller A., Merz H.,
"Expression of MDL-1
Submitted (JAN-2000)
                                                                                                                                                                                                                                                                                                                      Similarity
                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ICEK 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POPY-CD94.
                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                         Query Match
Best Local S
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Q8MJI3
                                                                                                                                                                                                                                                                                                                                   Matches
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                                                                                                                                                       SRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCA-DKGSHLLTFPDNQGVNLFQEYVGEDFY 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 WIGLRDIDG--WRWEDGPALSLSI-LSNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                        CSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42 SSCPDDWIGYQTKCYFISKKTKNWTLAQSFCSKHHGATLALLESKEDMVFLKQHVGRAEH
                                                                                                            15 ELPANPGCVHSKEHSIKATL----IWRLFFLIMFLTIIVCGMVAALSAIRANCHQEPSV
                                                                                     11 BLPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLL--LYQRTLCCGSKGFM
                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.

Yim D., Sotiriadis J., Kim K.-S., Shin S.-C., Jie H.-B.,
Rothschild M.F., Kim Y.B.;
"Molecular cloning, expression pattern, and chromosomal mapping of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human).
Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
Sus.
                                                             10;
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                                     Length 154;
                                                            67; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF484234; AAL91547.1; -... AP484234; AAL91547.1; -... AC, 0005529; F: sugar binding; IEA.
InterPro; IPR001304; Lectin_C;
Pfam; PF00059; lectin_c; 1... SMART; SM00034; CLECT; 1... TYPE LECTIN 2; 1... PROSITE; PS6014; C TYPE LECTIN 2; 1... SEQUENCE 159 AA; 18056 MW; Ā19C3EEBAE92AA69 CRC64;
            154 AA; 17728 MW; 7771926F318C038D CRC64;
                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata,
Mammalia, Eutheria, Cetartiodactyla, Suina, Suidae,
                                                                                                                                                                                                                                                                                                       01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Type II membrane protein CD69 splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                  15.4%; Score 160; DB 4; 28.6%; Pred. No. 4.3e-09; iive 23; Mismatches 67;
                                                                                                                                                                                                                                                                                  159 AA
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                                                                                                                                                                                         129 DFYWIGLRDIDG--WRWEDG 146
                                                                                                                                                                                                                  129 SDHWIGLSREQĞQPWKWING 148
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                                                             Conservative
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                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                           Sus scrofa (Pig)
                                                            40;
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                                  Query Match
            SEQUENCE
                                                 Local
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71 QC--SRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGE 128
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MEDLINE=22072192; PubMed=12077248;

Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;

Guethlein L.A., Flodin L.R., Adams E.J., Parham P.;

Species for Tracking the Coevolution of Killer Cell Ig-Like Receptors with MHC-C.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -----KGFMCS
                                                                                                                                                       MEDLINE-99380598; PubMed=10449773;

Bakker A.B., Baker E., Sutherland G.R., Phillips J.H., Lanier L.L.;

"Mycloid DAPL2-associating lectin (WDL)-1 is a cell surface receptor involved in the activation of mycloid cells.";

Proc. Natl. Acad. Sci. US.A. 96:9792-9796(1999).

EMBL; AJZ17684; CAB71334.1; -..

EMBL; AJZ17684; CAB71334.1; -..

GO; GO:0007157; P: sugar binding; IEA.

GO; GO:0007157; P: heterophilic cell adhesion; IEA.

InterPro; IPR001364; Lectin. C.

SMART; SM00034; CLECT. 1.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Pongo.
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Feller A.C.; in human blood and cell lines."; to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      188 AA; 21521 MW; 94A2DBD520DC1985 CRC64;
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01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15.4%; Score 159.5; DB 4 25.5%; Pred. No. 6.2e-09; iive 31; Mismatches 65
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7;
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                                                                                                                                                                                                                24 WKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCG----SKGFMCSQCSRCPNL 78
                                                                                                                                                       10 WLISGTLGIICLS--LMATLGILLKNSFTKLSIEPAFTPGPDIELQKD---SDCCSCQEK 64
                                                                                                                                                                                                                                                      Query Match 15.3%; Score 158.5; DB 6; Length 179; Best Local Similarity 26.7%; Pred. No. 7.5e-09; Matches 47; Conservative 26; Mismatches 84; Indels 19; Gaps
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
PROSITE; PS00022; EGF_1; 1.
Receptor.
SEQUENCE 179 AA; 20566 MW; 6752CB9F0F9A2609 CRC64;
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Search completed: August 10, 2004, 16:44:03 Job time : 32 secs

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August 10, 2004, 16:35:35; Search time 47.5 Seconds (without alignments) 1118.293 Million cell updates/sec
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1036
1 MADNSIYSTLELPAAPRVQD......GLHASSCEVALQWICEKVLP 188
                                                                                                                                                                                                                                                                                                       1082526
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
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Maximum Match 100%
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 188
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Mammall 7 Rat ma 1 Rots ma 8 Rots ma 7 Human 7 Human 9 Human 9 Human 9 Human 9 Human 9 Human 9 Human 9 Human 1 Human 1 Human 1 Human 1 Human 1 Human 1 Human 1 Human 1 Human 1 Human 1 Human 1 Human 1 Human 1 Human 1 Human 1 Human	Adwo4/91 Human Kp4
SUMMARIES	AAR77033 AAR88277 AAB8277 AAB8277 AAN89267 AAN99267 AAU00673 AAM9296 AAM9296 AAM92096 AAM90302 AAM90302 AAM90302 AAW972746 AAW272446 AAW772446 AAW8675 AAW8675 AAW8675	TC/FONEN
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Score	1036 1036 1036 1036 838 838 140 170 164.5 164.5 163.5	1
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179 2 AAW40222 179 8 ADE76965 162 6 AB0325543 140 4 AAU19836 140 4 AAU19836 140 4 ABB15422 140 5 ABB17809 140 5 ABP47805 140 7 ADC10872 140 7 ADC10118 140 7 ADC10118 149 2 AAW75877 149 2 AAW75877 149 2 AAW5592 149 2 AAW5877 149 2 AAW5877 149 2 AAW75877 149 2 AAW75877 149 2 AAW75877 149 2 AAW75877 149 2 AAW75877 149 2 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW75877 149 3 AAW72822	Aaw40222 CD94. 7/1	Ade76965 Human pro	Abo32543 Secreted	Abo32535 Secreted	Aau19836 Human nov	Aau19690 Human nov	Abb15422 Human ner	Abbi7909 Human ner	Abp48056 Human pol	Human	Human	Adc11018 Human pro	Aaw64544 Human lym	Aaw75877 Type II m	Aaw85592 Human C-t	Abb09713 Amino aci	Adc38674 Human sec	Aaw63013 Mouse dec	Aau72822 Human NKG	Aau72821 Human NKG
110000444444414111111111111111111111111	AAW40222	ADE76965	ABO32543	AB032535	AAU19836	AAU19690	ABB15422	ABB17909	ABP48056	ABP47910	ADC10872	ADC11018	AAW64544	AAW75877	AAW85592	ABB09713	ADC38674	AAW63013	AAU72822	AAU72821
	79 2	~	_	162 6	40 4	40 4	40 4	40 4	40 5	40 5	40 7	40 7	49 2	•	•		•	126 2	133 5	143 5
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0.0000000000000000000000000000000000000	155	155	154	154	153.5	153.5	153.5	153.5	153.5	153.5	153.5	153.5	153.5	153.5	153.5	153.5	153.5	153	153	153
	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAR77033 standard; protein; 188 AA.

AAR77033

Mast cell function-associated antigen, MAFA, soluble, ligand, identification; screening; inflammation; inflammatory; allergy; allergic; prevention. Novel DNA encoding a mast cell function-associated antigen (MAFA) - useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions. A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in combination with the MAFA to prevent inflammatory and allergic reactions Length 188; Mammalian mast cell function-associated antigen (MAFA). Query Match 100.0%; Score 1036; DB 2; Best Local Similarity 100.0%; Pred. No. 1.8e-96; Matches 188; Conservative 0; Mismatches 0; Claim 12; Page 37; 54pp; English. Tal M; (YEDA) YEDA RES & DEV CO LID. (RYCU/) RYCUS A. 94IL-00109257. 95WO-US004258. (first entry) Pecht I, Guthmann MD, WPI; 1995-366356/47. N-PSDB; AAT01471 Sequence 188 AA; Rattus rattus. W09527734-A1. 06-APR-1995; 08-APR-1994; 19-0CT-1995. 01-FEB-1996 AAR77033;

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Gaps

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Indels

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180
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                                                       120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the amino acid sequence of rat mast cell function-associated bartigen (MAPA), a type II membrane glycoprotein found on mast cells and basophils. The invention relates to cloning of the human MAPA molecule (see AAW88265) and to the discovery of splice variants (see AAW88266-67) of human MAPA that are not found in rat. Polypeptides and synthetic peptides (see AAW88256-64) based on human MAPA and human truncated MAPA, and polynucleotides encoding them, can be used in methods for the treatment of inflammatory and allergic diseases (e.g. rheumatoid
9
                1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                          CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN
                                                       CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN
                                                                                                               LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ
MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                                                                                                                                                                                                                         Mast cell function-associated antigen; MAFA; splice variant; rat; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
                                                                                                                                                                                                                                                                                                                                                              cell function-associated antigen (MAFA).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82. .84
/note= "Asn is N-glycosylated"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                       AAW88277 standard; protein; 188 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96.
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arthritis and asthma), and tumour growth

Sequence 188 AA;

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The present invention relates to a pharmaceutical composition comprising an agent which specifically binds to a mast cell function associated antigen (MARA) ligand on a target cell, and prevents or inhibits natural killer (NK) - or T-cell-expressed cell surface MARA from binding to MARA tigand and a pharmaceutically acceptable excipient. The invention is useful for inhibiting an NK- or T-cell-expressed cell surface MARA binding to a ligand on a target cell, by contacting the pharmaceutical composition in vitro, ex vivo or in vivo by administering the composition and amount sufficient to inhibit cell surface MARA binding to the ligand on the target cell. The agent or the composition is useful for treating a newour by stimulating the cyctoxic activity of an NK cell or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell- or TL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is rat MARA protein
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                                                                                                                                   120
                                                                                                                                                        180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pharmaceutical composition for treating tumor by stimulating cytotoxic activity of natural killer cell or T-cell, comprises an agent that binds to mast cell function-associated antigen ligand on target cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat; pharmaceutical composition; mast cell function associated antigen; MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL; immunosuppressive; cytostatic.
                                                                                                                                    CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN
                                                                1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                 1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                                   LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ
                                  Gaps
                                  ;
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   Length 188;
                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mast cell function associated antigen (MAFA) protein.
   5;
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Score 1036; DB 2;
Pred. No. 1.8e-96;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                         AAE11761 standard; protein; 188 AA.
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                                  0;
 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Takahashi N, Mikayama T;
                                  188; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GEMI-) GEMINI SCI INC.
                                                                                                                                                                                                                                                                                                     188
                                                                                                                                                                                                                                                                        WICEKVLP 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-611482/70.
                 Similarity
                                                                                                                                                                                                                                                                                                     WICEKVLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAD18736
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   Query Match
Best Local
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to the subject, to NK or T-cell or the target cell e.g. tumour cell, in an amount sufficient to inhibit cell surface MAFA binding to the ligand on the target cell. The agent or the composition is useful for treating a tumour by stimulating the cytotoxic activity of an NK cell or a cytotoxic T-cell (CTL), where the tumour comprises an NK cell- or CTL-susceptible tumour cell. The invention is also useful for inhibiting an activity of NK cell or a T-cell. The present sequence is mouse MAFA protein
                                                                                                                                                                                                                                                                                                                                                                                               CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALO 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mast cell function-associated antigen, MAFA, soluble, ligand, identification, screening, inflammation, inflammatory, allergic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel DNA encoding a mast cell function-associated antigen (MARA) - useful for screening for ligands of MAFA which are useful for prevention of inflammatory and allergic reactions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A soluble form of mast cell function-associated antigen (MAFA) can be produced by recombinant techniques for use in the ligand- screening assay. The ligands that are identified may be used alone or in combination with the MAFA to prevent inflammatory and allergic reactions
                                                                                                                                                                                                                                                                                                                                                    1 MADSSIYSTLELPEAPQVQDESRWKLKAVLHRPHLSRFAMVALGLLTVILMSLLMYQRIL
                                                                                                                                                                                                                                                                                                          1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Partial sequence of mast cell function-associated antigen (MAFA)
                                                                                                                                                                                                                                                               21; Indels
                                                                                                                                                                                                                     80.9%; Score 838; DB 4;
80.7%; Pred. No. 1.9e-76;
                                                                                                                                                                                                                                                               15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR77472 standard; protein; 114 AA.
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Matches 151; Conservative
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                                                                                                                                                                            Sequence 188 AA;
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                                                                                                                                                                                                                                      CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                         LPQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180
                                                                                                                                                                                                                                                                                                                                                         LICENYWGEDFYWIGLRDIDGWRWEDGPALSISILSNSVVQKCGTIHRCGIHASSCEVALQ 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse; pharmaceutical composition, mast cell function associated antigen, MAFA; natural killer cell; NK; tumour; therapy; cytotoxic T-cell; CTL;
                                                                                                                                                                                                                                                                             CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
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                                                                                                                                                                                     1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                                                 1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
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                                                                 Length 188;
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                                                                                                           Indels
                                                                 DB 4;
L.8e-96;
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                                                                                     Pred. No. 1.8
Mismatches
                                                              100.0%; Score 1036; 100.0%; Pred. No. 1.
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                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                WICEKVLP 188
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                                                                                  Local Similarity
es 188; Conser
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                      Sequence 188
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Domain

Key

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CCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVN 120
                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                                                                                                                                                                      AAU00673 standard; protein; 165 AA.
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                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                          'note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-308477/32.
                                                                                            181 WICEKV 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cellular processes.
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                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
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                                                                                                                                                                                             AAU00673;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New polypeptide having a sequence corresponding to human mast cell function-associated antigen - useful in forming and manufacturing pharmaceutical compositions in the treatment of inflammatory and allergic
                                                                        CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This is the amino acid sequence of human mast cell function- associated antigen (MAFA) splice variant huMAFA(E3/4-), which lacks the C-lectin-like domain of human MAFA (see AAMW8826) but retains the intracellular and transmembrane domains as well as the extracellular C-terminal tail. Truncated MAFA polypeptides including huMAFA(E3/4-), and polynucleotides encoding them, as well as synthetic peptides (see AAW88258-64, AAW88268-72), can be used be used in compositions for the treatment of inflammatory and allergic diseases (e.g. rheumatoid arthritis and asthma), or tumour growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
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                                                    Gaps
                                                                                                                   LRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQWICEKVLP 188
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                                                                                                                                                                                                                                                                                Mast cell function-associated antigen; MAFA; huMAFA(E3/4-); splice variant; human; inflammation; allergy; asthma; rheumatoid arthritis; tumour; therapy.
                             Length 114;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          30; Indels
                                                   Indels
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Pred. No. 4.7e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Williams DH;
                                                    ö
                                        8.1e-58;
                              DB 2;
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29.6%; Pred. No. 4...
...
12; Mismatches
                       62.8%; scor.
100.0%; Pred. No. cor.
... 0; Mismatches
                                                                                                                                                                                                                                                          Human MAFA splice variant huMAFA(E3/4-).
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                                                                                                                                                                                             A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 3; 44pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                    (PEPT-) PEPTIDE THERAPEUTICS LTD.
                                                                                                                                                                                             AAW88267 standard; protein; 99
                                                                                                                                                                                                                                                                                                                                                                                          98WO-GB001572.
                                                                                                                                                                                                                                                                                                                                                                                                                 97GB-00011148.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases, and tumour growth.
                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lamers MBAC,
                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-059806/05.
N-PSDB; AAV84200.
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                                        Similarity
          Sequence 114 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 99 AA;
                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                WO9854209-A2
                                                                                                                                                                                                                                                                                                                                                                                          29-MAY-1998;
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                                                   Matches 114;
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                                                                                                                                                                                                                AAW88267;
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                              Query Match
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The sequence represents human INTERCEPT 289 form 2a polypeptide. This protein and similar others exhibit the ability to affect growth, proliferation, survival, differentiation, activity, morphology, or movement/migration of, e.g. T cells and cells of the heart, liver, pancreas, placenta, brain, lung, skeletal muscle, kidney, spleen, lymph node, peripheral blood leukocyte, bone marrow or thymus tissue. They can be used as modulating agents for regulating cellular processes, thus, the proteins and their associated nucleic acids can be used to prognosticate, prevent, diagnose, or treat disorders associated with physiological processes. These disorders include abnormal blood coagulation, asthma, anaphylaxis, hepatitis, multiple sclerosis, cancer, coronary artery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated nucleic acid molecule for diagnosis, prevention, and therapy of human and other animal disorder, or as modulating agent for regulating
121 LFQEYVGEDFYWIGLRDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGLHASSCEVALQ 180
                                                                                                                  --ISSNSFVQTCGALTKNGLQASSCEVPLH 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; INTERCEPT 289; T cell; heart; liver; pancreas; placenta; brain; skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte; bone marrow; thymus tissue; abnormal blood coagulation, asthma; cancer; anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; malaria; atopic dermatitis; amyotrophic lateral sclerosis; meningitis; attention deficit disorder; Crohn's disease; gastroenteritis; goltre; hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism; muscular dystrophy; immuno-competence; vertebrate; blood; serum; lung.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fraser CC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human INTERCEPT 289 form 2a polypeptide.
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hormonal disorder; proliferative disorder; cancer; thyroid disorder;
diabetes; multiple sclerosis; lupus; neurological disorder; anaemia;
Alzheimer's disease; Parkinson's cardiovascular disorder;
myocardial infarction; congestive heart disease; blood platelet disorder;
thrombocytopenia; blood vessel; atherosclerosis; vasculitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92 EKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RDIDGWRWEDGPA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SESSWINESRDFCKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWRWINNSV 124
disease, malaria, atopic dermatitis, amyotrophic lateral sclerosis, meningitis, attention deficit disorder, Crohn's disease, gastroenteritis, goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary embolism and muscular dystrophy. Antibodies to disorders such as these can be made by providing a polypeptide of the invention to an immunocompetent vertebrate and harvesting blood or serum from the vertebrate
                                                                                                                                                                                                                                                                                                                                                                  40 MVALGLLTVIL-----MSLLLYQRTLCCGSKGFMCSQC--SRCPNLWMRNGSHCYYFSM 91
                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                 18;
                                                                                                                                                                                                                                                     Score 170; DB 4; Length 165;
Pred. No. 5.5e-09;
                                                                                                                                                                                                                                                                                                           68; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        149 LSLSILSNSVVQKCGTIHRCGL----HASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                           31; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Secreted polypeptide-related protein #24.
                                                                                                                                                                                                                                                       16.4%; Score 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABO32541 standard; protein; 165 AA
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10-SEP-1999; 99US-00393996.
19-OCT-1999; 99US-00420707.
07-JAN-2000; 2000US-00479249.
27-APR-2000; 2000US-00559497.
24-MAX-2000; 2000US-00558063.
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                                                                                                                                                                                                                                                                                 27.38;
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                                                                                                                                                                                                                                                                                                           Conservative
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GOODEARL A D
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BARNES T M.
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KIRST S J.
MYERS P S.
LEIBY K R.
                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                 Sequence 165 AA;
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(BARN/)
(SHAR/)
(KIRS/)
(MYER/)
                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (LEIB/)
(HOLT/)
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(MACK/)
(GOOD/)
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                                                                                                                                                                                                                                                                                                         Matches
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The invention relates to secreted polypeptide-related proteins and nucleic acids (TANGO and INTERCEPT proteins and nucleic acids). The nucleic acids, proteins and antibodies specific to the proteins are nucleic acids, proteins and antibodies specific to the proteins are useful in screening assays, predictive medicine (e.g. diagnostic assays, prophostic assays, monitoring clinical trials and pharmacogenetics) and prophylactic and therapeutic methods. The sequences are used in diagnosing, preventing or treating proliferative disorders (e.g. annutiple sclerosis or lugus), neurological disorders (e.g. multiple sclerosis or lugus), neurological disorders (e.g. Alzheimer's disease or Parkinson's disease), cardiovascular clisorders (e.g. thromboytopenia or ansemia) and disorders involving blood vessels (e.g. thromboytopenia or ansemia) and disorders acids may also be used in chromosome mapping, tissue typing and forensic clology, and as surrogate markers. This sequence represents a secreted polypeptide-related protein of the invention. Note: The sequence data for this patent was obtained in electronic format directly from USPTO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Š.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 EKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RDIDGWRWEDGPA 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              65 SESSWNESRDFCKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWRWINNSV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted extracellular matrix protein; immunomodulatory; Anti-HIV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  40 MVALGLLTVIL-----MSLLLYQRTLCCGSKGFMCSQC--SRCPNLWMRNGSHCYYFSM 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antianemic; antirheumatic; antisclerotic; cardiant; vascular; cerebroprotective; thrombolytic; antimicrobial; ophthalmic; cytostatic; antialzheimers; immuned autoimmune disease; HIV infection; anaemia; human immunodeficiency virus; rheumatoid arthritis; multiple sclerosis; cancers; hyperproliferative disorder; breast neoplasm; melanoma;
                                                                                                                                           New nucleic acid molecule encoding a secreted protein (e.g. TANGO 202, TANGO 210 or INTERCEPT 217), useful for diagnosing, preventing or treating disorders such as cancer, diabetes or atherosclerosis, and in forensic biology.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sezary syndrome; Gaucher's disease; neurological diseases;
Alzheimer's disease; Parkinson's disease; cardiovascular disorder;
cardiac arrest; tachycardia; angina; infection; corneal infections;
wound healing; immunogen; gene therapy; antisense; food additive.
                  Sharp JD, Kirst SJ, Myers PS, Leiby KR;
SA, Wrighton N, Mackay CR, Goodearl ADJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human novel extracellular matrix protein, Seg ID No 310.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LSLSILSNSVVQKCGTIHRCGL----HASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125 FNGNVTNQNQNFNCATI ---GLIKTFDAASCDISYRRICEK 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16.4%; Score 170; DB 6; 27.3%; Pred. No. 5.5e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31; Mismatches
                                                                                                                                                                                                                                                        Claim 9; Fig 11H-11K; 482pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seqdata.uspto.gov/sequence.html
                                                                                 WPI; 2003-456290/43.
N-PSDB; ACD66723, ACD66724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 27.3% nes 44; Conservative
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                                        Mccarthy
                  Barnes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 165 AA;
      cc,
DA,
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                                        Holtzman
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2000US-023703P

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2001US-0259678P
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08-NOV-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
01-DEC-2000;
05-DEC-2000;
05-DEC-2000;
06-DEC-2000;
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08-DEC-2000;
08-DEC-2000;
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27-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
13-OCT-2000;
13-OCT-2000;
13-OCT-2000;
20-OCT-2000;
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08-NOV-2000;
08-NOV-2000;
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2000US-0186628P.
2000US-018664P.
2000US-0186364P.
2000US-0189874P.
2000US-0198123P.
2000US-0198123P.
2000US-025515P.
2000US-0217487P.
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25-SEP-2000;
26-SEP-2000;
  Homo sapiens
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US2002042386-A1.
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                                                                                                                                                                             The invention relates to isolated nucleic acid molecules encoding novel human secreted extracellular matrix proteins (SPS). The polynucleotides and proteins are used to prevent, treat a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. For example, disorders associated with decreased expression of SPs. The SP polynucleotide or a vector expressing them may be administered to treat diseases by gene therapy. Antisense molecules may be administered to down regulate expression of SPs by binding with the cells own genes and preventing their expression. The polynucleotides may also be used as DNA probes in diagnostic assays. The SPs may also be used as DNA probes in diagnostic assays. The SPs may also be used as DNA
                                                                                                                                                                                                                                                                                                                                    produce antibodies and to identify modulators (agonists and antegonists) of the SPs. The anti-(SP) antibodies and antagonists may also be used to demonstrate the SPs. The anti-(SP) antibodies and antagonists may also be used to deven regulate expression and activity of SP and as diagnostic agents for example: immune/autoimmune diseases (E.g. HIV (human immunodeficiency virus) infections, anaemia, rheumatoid arthritis and multiple sclerosis), cancers and hyperproliferative disorders (E.g. melanomas, neoplasms of the breast or liver, Sezary syndrome and Gaucher's disease), neurological diseases (E.g. Alzheimer's disease, Parkinson's disease), neurological /cerebrovascular disorders (E.g. cardiac arrest, tachycardia and angina), infections caused by bacteria, viruses and fungi and ocular disorders (E.g. corneal infections). Other uses include wound healing, maintenance of organs before transplantation, support of cell culture of primary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CASRS--ADQIVLCQSEWLKYQGKCYWPSNEMKSWSDSYVYCLERKSHLLIIHDQLEMAF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FQEYVGE-DFYWIGLRDID---GWRWEDGPALSLSIL-----SNSVVQKCGTIHRCGL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     112 IQKNLRQLNYVWIGLNFTSLKMTWTWVDGSPIDSKIFFIKGPAKENS----CAAIKESKI 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; nootropic; neuroprotective; cytostatic; dermatological; virucide; immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnerary; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antirheumatic; hepatotropic; cerebroprotective; antiinflammatory; antiallergic; antidiabetic; antiulcer; anticonvulsant; antifungal; antiparasitic; cardiant; immune disorder; cardiovascular disorder; neurological disease; infection; nephrotropic; gene therapy; vaccine.
                                                                                      Nucleic acid molecules encoding human secreted extracellular matrix proteins, used in preventing, treating or ameliorating a disorder, e.g. Alzheimer's and Parkinson's diseases and cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 4; Length 182;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15.9%; Score 164.5; DB 4 26.9%; Pred. No. 2.2e-08; tive 22; Mismatches 59
                                                                                                                                                   Claim 11; SEQ ID NO 310; 577pp; English.
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            Ruben SM;
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            Barash SC,
                                           WPI; 2001-465572/50
                                                       N-PSDB; AAS31231
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            Rosen CA,
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nucleic acid encoding human proteins, useful for diagnosis, treatment prevention of e.g. osteoporosis, also related polypeptides and
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        medical conditions e.g. by protein or gene therapy. The genes are solated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (ant) agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and oversam cancer and other cancers of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung, or unogenital; (b) immune disorders e.g. Addison's disease, allergies, autoimmune heamolytic can anemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c) cardiovascular disorders such as myocardial isobaemias; (d) wound healing (e) infectious diseases such as viral, bacterial, fungal and parasitic infections. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly
                                                                                                                                                                                                                                                                                                                          54 CASRS--ADQTVLCQSEWLKYQGKCYWFSNEMKSWSDSYVYCLERKSHLLIHDQLEMAF 111
                                                                                                                                                                                                                                                                                                                                                               122 FQEYVGE-DFYWIGLRDID---GWRWEDGPALSLSIL-----SNSVVQKCGTIHRCGL 170
                                                                                                                                                                                                                                                                                                                                                                                CGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                neuroprotective; gynaecological; gastrointestinal-Gen; cardiant; cardiovascular-Gen; nephrotropic; antiinflammatory; muscular-Gen; respiratory-Gen; immunosuppressive; cerebroprotective; vasotropic; nootropic; antiallergic; cancer; bacterial infection; viral infection; neural disorder; immune system disorder; blood disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; pulmonary disorder; cardiovascular disorder; renal disorder;
                                                                                                                                                                                                                                                        Query Match 15.9%; Score 164.5; DB 5; Length 182; Best Local Similarity 26.9%; Pred. No. 2.2e-08; Matches 36; Conservative 22; Mismatches 59; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Extracellular matrix protein; cytostatic; antibacterial; virucide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inflammatory disorder; proliferative disorder; Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human extracellular matrix protein from gene 35
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04-FEB-2000; 2000US-0184664P.
02-MAR-2000; 2000US-0184664P.
16-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-0199874P.
18-APR-2000; 2000US-0199123P.
19-MAY-2000; 2000US-020515P.
07-JUN-2000; 2000US-0205515P.
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                                                                                                                                                                                                                               Sequence 182 AA;
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Claim 11; SEQ ID NO 310; 235pp; English.
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2000US-0249210P.
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2000US-0249211P.
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2000US-0249217P.
2000US-0249218P.
2000US-0249244P.
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2000US-0251030P.
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2000US-0246474P.
2000US-0246475P.
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2000US-0249214P.
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2000US-0250160P.
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2000US-0251479P.
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2000US-0251868P.
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                         2000US-0241809P.
                                                                                                             2000US-0246525P.
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                                                                                     2000US-024647BP
                                                                                            2000US-0246523P
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05-DEC-2000; 2
06-DEC-2000; 2
08-DEC-2000; 2
20-0CT-2000; 2
8-NOV-2000; 2
17-NOV-2000; 2
11-NOV-2000; 2
11-NOV-2000; 2
11-NOV-2000; 2
11-NOV-2000; 2
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01-DEC-2000; 2
01-DEC-2000; 2
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17-NOV-2000;
17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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17-NOV-2000;
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08-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rosen CA,
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The invention relates to an isolated nucleic acid molecule (cDNA) encoding a human extracellular matrix protein, representing one of 161 novel genes. Also include are recombinant vectors, host cells (expressing the protein), the extracellular matrix proteins (including
New isolated nucleic acids and polypeptides, useful for diagnosing, treating, and/or preventing disorders, such as cancer, infections, cardiovascular and inflammatory diseases.
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their fragments, epitopes and homologues), an isolated antibody that binds specifically to the protein, diagnosing a pathological condition or susceptibility to a pathological condition (comprising determining the presence or absence of a mutation in the mucleic acid and diagnosing a condition based on the presence or absence of the mutation), diagnosing a pathological condition or susceptibility to a pathological condition or condition or susceptibility to a pathological condition or protein in a biological sample and diagnosing a condition based on the protein in a biological sample and diagnosing a condition based on the protein in a mammalian subject, identifying a binding partner to the protein to a mammalian subject, identifying a binding partner to the protein, the gene corresponding to the cDNA sequence, and identifying an ectivity in a biological sassy (comprising expressing the nucleic acid in a cill, isolating the supernatant, detecting an activity in a biological cassy and identifying the protein in the supernatant having the activity. The nucleic acids and proteins display the following activity. The nucleic acids and proteins display the following activities Cytostatic, antibacterial, viruciach, Neuroprotective, Gymaecological, Gastointestinal-den, Cardiant, Cardiovascular-Gen, Nephrotropic, Antiinflammatory, Muscular-Gen, Respiratory-Gen,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 FQEYVGE-DFYWIGLRDID---GWRWEDGPALSLSIL-----SNSVVQKCGTIHRCGL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 CGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFFDNQGVNL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, cytokine; cell proliferation; cell differentiation; gene therapy; vaccine; peptide therapy; stem cell growth factor; haematopoiesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                        Indels 17; Gaps
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Wang ;
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Chen R, V
                                                                                                                                                                                                                                                                                                                                                                                     Length 182;
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Pang D, Wang J, Zhang J, Ren F,
                                                                                                                                                                                                                                                                                                                                                                                     15.9%; Score 164.5; DB 7; 26.9%; Pred. No. 2.2e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                            59;
                                                                                                                                                                                                                                                                                                                                                                                                                            22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAM80296 standard; protein; 142 AA.
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2000US-00560875.
2000US-00598075.
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01-SEP-2000; 2000US-00654936.
15-SEP-2000; 2000US-006549361.
20-OCT-2000; 2000US-0069325.
30-NOV-2000; 2000US-00728422.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 HASSCEVALOWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FSETCSSVFKWICQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            36; Conservative
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Ma Y, Zhao QA, Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200157190-A2.
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20-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Yang Y;

Wehrman T,

Asundi V,

Liu C,

Goodrich R,

Zhou P,

DRMANAC R T. ASUNDI V. WEHRMAN T.

YANG

TANG Y T. ZHOU P. GOODRICH R

LIU C.

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03-FEB-2000; 2000US-00496914.
27-APR-2000; 2000US-00560875.
                                                                                                                                                                                                   Drmanac RT;
                                                                                                                                       (YANG/)
(DRMA/)
                                                                                                                                                                                   Tang YT,
                                                             (ZHOU/)
(GOOD/)
                                                                                                         (ASUN/)
(WEHR/)
                                               (TANG/)
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                                                                                                                                                                                        production of other cytokines in other cell populations. The populations of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, hematopoiesis regulating activity, issue growth factor activity, immunomodulatory activity and activity, inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581) 2111

(AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                  The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        wound; ulcer; thrombocytopaenia; osteoporosis; osteoarthritis; inflammation; Alzheimer's disease; Parkinson's disease; stroke; Huntington's disease; amyotrophic lateral sclerosis; HUV; immune deficiency; human immunodeficiency virus infection; severe combined immunodeficiency; infection; autoimmune disorder; rheumatoid arthritis; Guillain-Barre syndrome; graft-versus-host disease; cancer; thyroid cancer; lung cancer; syndrome; graft-versus-host disease; Kaposi's sarcoma; brain tumour; prostate cancer; ovarian cancer; chu, disorder; inflammatory bowel disease; chu, disorder; inflammatory bowel disease;
                                                                        Nucleic acids encoding polypeptides with cytokine-like activities, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             49 ASQAFCSAYHATLPLLISHTQ--DFLGRYPVSRHSWVGAWRGPQGWHWIDEAPLPPQLLPB 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98 SSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL-RDIDGWRWEDGPALSLSIL-- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                        38 LVMVALGLITVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 VLLAVSGVVIVVLASR------AGAR------CQQCPPGWVLSEHCYYFSAEAQAWE 48
                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytokine; cell proliferation; cell differentiation; anaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human cytokine or cell proliferation/differentiation protein #6.
                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                               15.8%; Score 163.5; DB 4; Length 142; 26.1%; Pred. No. 2.1e-08; ive. 25; Mismatches 67; Indels 21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DGEDNLDINCGALEEGTLVAANCSTPRPWVCAK 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --SNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
Goodrich R;
                                                                                                                    Claim 20; Page 6210-6211; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABG72616 standard; protein; 142 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Crohn's disease; food supplement.
Yang Y, Wejhrman T,
                                                                                        diagnosis and gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  30-JAN-2001; 2001US-00774434.
                                                                                                                                                                                                                                                                                                                                                                                            Query Match 15.89
Best Local Similarity 26.15
Matches 40; Conservative
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                            2001-476283/51.
                                            N-PSDB; AAK53429
                                                                                                                                                                                                                                                                                                                                                                 Sequence 142 AA;
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Xue AJ,
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The invention relates to an isolated polynucleotide encoding a cytokine or cell proliferation/differentiation-related protein (or the mature protein or active domain), sequences greater than 90% identical to it or sequences complementary to it. Also included are the encoded proteins, expression vectors, transformed host cells, antibodies, and identifying a compound that binds to the polypeptide. The polynucleotide, polypeptides compound that binds to the polypeptides are useful in therapeutic, diagnostic or research methods. They are particularly useful crampedicial treating or preventing e.g. anaemias, wounds, ulcers, thrombocytopeania, osteoporosis, osteoarthritis, inflammations, continued or preventing e.g. anaemias, wounds, ulcers, thrombocytopeania, osteoporosis, osteoarthritis, inflammations, amyotrophic lateral sclerosis, stroke, immune deficiencies (e.g. human immunodeficiency virus (HIV), severe combined immunodeficiency or infections), autoimmune disorders (e.g. rheumatoid arthritis, Guillain-cancer, lung cancers, small cell carcinoma, Kaposi's sarcoma, brain cuncers, prostate cancer, ovarian cancer or leukaemias), or inflammatory disorders (e.g. inflammatory bowel disease or Crohn's disease). The polymucleotides and proteins are useful for screening peptides or small cell cancell inhibitors or agonists that are useful for treating these diseases. The polypeptide is also useful as molecular markers, or as a food supplement. The present sequence is a cytokine or cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ŋ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           49 ASQAFCSAYHATLPILISHTQ--DFLGRYPVSRHSWVGAWRGPQGWHWIDEAPLPPQLLPE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 VLLAVSGVVIVVLASR----AGAR-----CQQCCPGWVLSEEHCYYFSAEAQAWE 48
                                                                                                                                      New polynucleotides for diagnosing, treating or preventing e.g. anemia, wounds, ulcers, thrombocytopenia, osteoporosis, inflammations, Alzheimer's disease, stroke, autoimmune disorders or cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38 LVMVALGLLTVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWN
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26.1%; Pred. No. 2.1e-08;
iive 25; Mismatches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 -- SNSVVQKCGTIHRCGLHASSCEVALQWICEK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::: | | : | | : | | 107 DGEDNLDINCGALEEGTLVAANCSTPRPWVCAK 139
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                                                                                                                                                                                                                                                                                                                      Claim 19; Page 60; 63pp; English.
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WPI; 2003-110596/10.
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Best Local Similarity
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                                                       N-PSDB; ABX13629
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Local Similarity
nes 45; Conserva
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                                                                                                                                                                                                                                                                                                                              Key
                   4AU0067
                              5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The production of other cytokines in other cell populations. The polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding polypeptides with cytokine-like activities, useful in diagnosis and gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98 SSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL-RDIDGWRWEDGPALSLSIL-- 154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ASOAFCSAYHATLPLLSHTO--DFLGRYPVSRHSWVGAWRGPQGWHWIDEAPLPPQLLPE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38 LVMVALGLLTVILMSLLLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWN 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; cytokine; cell proliferation; cell differentiation; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Cao Y;
R, Wang ZW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                        vaccine; peptide therapy; stem cell growth factor; haematopolesis; tissue growth factor; immunomodulatory; cancer; leukaemia; nervous system disorder; arthritis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Xu C, ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Zhou P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
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JJ, Zhang J, J
Goodrich R;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 20, Page 477; 6221pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Drmanac RT,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wejhrman T,
                                                                                                                                                                                                                                                                             27-APR-2000; 2000US-00560875.
20-UIN-2000; 2000US-00596075.
19-UUL-2000; 2000US-005235.
01-SIP-2000; 2000US-00654936.
15-SIP-2000; 2000US-00663561.
                                                                                                                                                                                                                                                                                                                                                           20-OCT-2000; 2000US-00693325.
30-NOV-2000; 2000US-00728422.
                              Human protein SEQ ID NO 3960.
                                                                                                                                                                                                                                   05-FEB-2001; 2001WO-US004098
(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wang D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-476283/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                        (HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yang Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-PSDB; AAK53435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Seguence 160 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Tang YT, Liu C
Ma Y, Zhao QA,
                                                                                                                                                                       WO200157190-A2
                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                  03-FEB-2000;
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Best Local S
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New isolated nucleic acid molecule for diagnosis, prevention, and therapy of human and other animal disorder, or as modulating agent for regulating
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                                                                                                                                                                                                                                                                                                                              Human; INTERCEPT 289; T cell; heart; liver; pancreas; placenta; brain; skeletal muscle; kidney; spleen; lymph node; peripheral blood leukocyte; bone marrow; thymus tissue; abnormal blood coagulation; asthma; cancer; anaphylaxis; hepatitis; multiple sclerosis; coronary artery disease; malaria; atopic dermatitis; multiple sclerosis; coronary artery disease; mattention deficit disorder; Crohn; disease; gastroenteritis; goltre; hypoglycaemia; diabetes mellitus; endometriosis; pulmonary embolism; muscular dystrophy; immuno-competence; vertebrate; blood; serum; lung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               goitre, hypoglycaemia, diabetes mellitus, endometriosis, pulmonary embolism and muscular dystrophy. Antibodies to disorders such as these can be made by providing a polypeptide of the invention to an immunocompetent vertebrate and harvesting blood or serum from the vertebrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.7%; Score 163; DB 4; Length 145; 28.5%; Pred. No. 2.4e-08; tive 25; Mismatches 56; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7. .28
/note= "Transmembrane domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Extracellular domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fraser CC,
                                                                                                                                                                                                                                                           Human INTERCEPT 289 form 3a polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8; Fig 2P-2Q; 263pp; English.
AAU00675 standard; protein; 145 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JUN-2000; 2000WO-US017386.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (MILL-) MILLENNIUM PHARM INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myers PS,
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40 MVALGLITVIL----MSL-LLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKR 94

Conservative

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(without alignments)
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1 MADNSIYSTLELPAAPRVQD......GLHASSCEVALQWICEKVLP
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Gapop 10.0 , Gapext 0.5
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    protein search,

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No. Score Match Length DB ID Description

1 1036 100.0 188 9 US-09-811-367B-5 Sequence 5, Appli 2 88.0 80.9 188 9 US-09-759-130B-98 Sequence 37, Appli 3 170 16.4 165 16 US-10-741-790-98 Sequence 38, Appli 5 167.5 16.2 161 10 US-09-76-51B-55 Sequence 98, Appli 6 164.5 15.9 182 9 US-09-76-51B-55 Sequence 55, Appli 6 164.5 15.9 182 19 US-09-76-51B-55 Sequence 310, Appli 164.5 15.9 182 19 US-09-76-51B-55 Sequence 100, Appli 164.5 15.9 182 19 US-09-76-51B-55 Sequence 100, Appli 164.5 15.9 182 19 US-09-76-10 Sequence 100, Appli 164.5 15.9 181 10 US-09-759-130B-108 Sequence 100, Appli 165.5 181 13 US-10-114-893-2 Sequence 22, Appli 165.5 15.4 188 10 US-09-759-130B-83 Sequence 23, Appli 169.5 15.4 188 10 US-09-759-130B-83 Sequence 83, Appli 169.5 15.4 188 10 US-09-759-130B-83 Sequence 83, Appli 169.5 15.0 179 10 US-09-919-039-130 Sequence 130, Appli 165 15.0 179 10 US-09-919-039-130 Sequence 130, Appli 165 15.0 179 10 US-09-919-039-130

Sequence 10, Appl Sequence 100, App Sequence 100, App		Sequence 340, App Sequence 486, App	a)	Sequence 486, App Segmence 11 Appl	Sequence 32, Appl	2	Sequence 1, Appli	m	7	90	86,	86,	Sequence 12, Appl	Sequence 466, App	Sequence 466, App	Sequence 6, Appli	Sequence 1275, Ap	Sequence 110, App	Sequence 110, App	Sequence 302, App	Sequence 302, App	Sequence 5855, Ap	Sequence 67, Appl	Sequence 836, App
.5 US-10-335-009-10 .0 US-09-759-130B-100 .6 US-10-741-790-100	10 US-09-759-130B-85 16 US-10-741-790-85	US-09-764-870-340 US-09-764-870-486	L4 US-10-125-540-340	14 US-10-125-540-486	L3 US-10-114-893-32	L4 US-10-088-859-2	L4 US-10-179-528-1	L2 US-10-239-656-3	12 US-10-239-656-2	12 US-10-239-656-90		16 US-10-741-790-86	16 US-10-775-640-12	9 US-09-764-870-466	14 US-10-125-540-466	9 US-09-944-807-6	12 US-10-296-115-1275	10 US-09-759-130B-110	16 US-10-741-790-110	9 US-09-764-8:70-302	14 US-10-125-540-302	14 US-10-106-698-5855	12 US-09-964-956-67	12 US-10-072-012-836
138	162 1	140	140 1	140	149	149 1	149	133	143	162	•		187	94	94	149	146 1	117	117	•	119	137	124	124
155 15.0 154 14.9 154 14.9	והה	153.5 14.8 153.5 14.8	153.5 14.8	153.5 14.8	153.5 14.8			153 14.8									146 14.1		145 14.0			144 13.9	142 13.7	
16 17 18	110 20	21	23	4.00	7 7 7	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Sequence 5, Application US/09811367B

Sequence 5, Application US/09811367B

Sequence 5, Application US/09811367B

Sequence 5, Application US/09811367B

GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Mikayama, Toshifumi
TITLE OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (MAFA)
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THER FILE REFERENCE: 021286/0278719
CURRENT FILING DATE: 2002-03-12
PRIOR FILING DATE: 2000-03-17
NUMBER OF SEQ ID NOS: 20
SOFFWARE: Patentin Version 3.0
SEQ ID NO 5.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Rattus norvegicus
US-09-811-367B-5
KESULT 1
US-09-811-367B-5
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APPLICANT: MCCARTLY, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Barnes, Thomas S
APPLICANT: Barnes, Thomas S
APPLICANT: Mirst, Susan J
APPLICANT: Mackay, Charles R
APPLICANT: Myers, Paul S
APPLICANT: Myers, Paul S
APPLICANT: Mighton, Nicolas
APPLICANT: Mighton, Nicolas
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: UGBS:
TITLE OF INVENTION: UGBS:
TITLE OF INVENTION: UGBS:
CURRENT FALLICATION NUMBER: US/10/741,790
CURRENT FALLICATION NUMBER: US/10/741,790
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16.4%; Score 170; DB 10; Length 165; 27.3%; Pred. No. 1.8e-09; ive 31; Mismatches 68; Indels 1
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PRIOR FILING DATE: 2000-01-07
PRIOR PLING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-29
PRIOR PRILORION NUMBER: US 09/596,194
PRIOR FILING DATE: 1999-06-29
PRIOR PRILORION NUMBER: US 09/42,364
PRIOR FILING DATE: 1999-06-39
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR PLING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR PLING DATE: 2000-06-30
PRIOR PRILOR DATE: 2000-06-30
PRIOR PRILOR DATE: 2000-06-31
PRIOR PLING DATE: 1999-010
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR PRILOR DATE: 1999-10-19
PRIOR SEQ ID NOS: 460
NUMBER OF SEQ ID NOS: 460
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PRIOR FILING DATE: 2000-01-07
PRIOR PELICHON NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
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Publication No. US20040121396A1
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 44; Conserv
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US-10-741-790-98
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APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Takahashi, No. US20020155110Aluaki
APPLICANT: Mikayama, Toshidumi
TITLA OF INVENTION: SOLUBLE MAST CELL FUNCTION ASSOCIATED ANTIGEN (WAFA)
TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS AND METHODS OF MAKING AND USING THEM FILE REPREMENTE: 0202-03-12
CURRENT APPLICATION NUMBER: US/09/811,367B
PRIOR PAPLICATION NUMBER: 03-17
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PATENT OF NUMBER: 2000-03-17
NUMBER OF SEQ ID NOS: 20
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
TITLE REPREBENCE: WP100-2350MINH
CURRENT APPLICATION NUMBER: US/09/759,130B
CURRENT APPLICATION DATE: 2002-09-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CCGSKDSTCSHCPSCPILWTRNGSHCYYFSMEKKDWNSSLKFCADKGSHLLTFPDNQGVK 120
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80.9%; Score 838; DB 9;
Best Local Similarity 80.7%; Pred. No. 9:7e-79;
Matches 151; Conservative 15; Mismatches 21
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                                                                                                                                                                                  Sequence 3, Application US/09811367B
Patent No. US20020155110A1
GENERAL INFORMATION:
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Kirst, Susan J
Mackay, Charles R
Myers, Paul S
Leiby, Kevin R
Wrighton, Nicolas
Goodearl, Andrew
        188
                                           181 WICEKVLP 188
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WICKKVL 187
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     181 WICEKVLP
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                                                                                                                                                                                                                                                                                                                                     16.2%; Score 167.5; DB 10; Length 161; 28.7%; Pred. No. 3.2e-09; ive 21; Mismatches 71; Indels 15;
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GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
TITLE REFRENCE: PTZ14
CURRENT APPLICATION NUMBER: US/09/764,870
CURRENT PILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 310
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Anti
FILE REFERENCE: PTZ14C1
CURRENT APPLICATION NUMBER: US/10/125,540
CURRENT FILING DATE: 2002-04-19
Prior Application removed - See File Wrapper or Palm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 310, Application US/09764870 Patent No. US20020042386A1
   PRIOR FILING DATE: 1999-06-30
NUMBER OF SEQ ID NOS: 85
SOFTWARE: Patentin version 3.1
SEQ ID NO 55
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ORGANISM: Homo sapiens
                                                                                                                                                                                                  TYPE: PRT ORGANISM: Homo sapiens
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Best Local Similarity
Matches 36; Conserv
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                                                                                                                                                          LENGTH: 161
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Matches
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APPLICANT: HOLTZMAN, Douglas A
APPLICANT: HOLTZMAN, Douglas A
APPLICANT: KHODADOUST, Mehran M
TITLE OF INVENTION: WOU'SL GENES ENCODING PROTEINS HAVING PROGNOSTIC, DIAGNOSTIC, PREV
TITLE OF INVENTION: THERAPEUTIC, AND OTHER USES
FILE REFERENCE: 10147-65
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CURRENT FILING DATE: 2002-05-07
PRIOR PEDILICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/33,159
PRIOR PELING DATE: 1999-06-16
PRIOR PELING DATE: 1999-06-16
PRIOR PILING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/342,364
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR PILING DATE: 1999-06-29
PRIOR FILING DATE: 2000-06-30
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PRIOR FILING DATE: 2000-05-24
PRIOR APPLICATION NUMBER: US 09/333,159
PRIOR PILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 1999-06-29
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR PILING DATE: 1999-09-10
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-31
PRIOR FILING DATE: 2000-06-31
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-01-01
PRIOR FILING DATE: 1999-01-01
PRIOR FILING DATE: 1999-10-13
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PRIOR FILING DATE: 1999-10-13
PRIOR FILING DATE: 1999-10-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 09/393,996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 55, Application US/09766511B Publication No. US20030170621A1 GENERAL INFORMATION:
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APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
APPLICANT: BARNES, Thomas
APPLICANT: KIRS, Thomas
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WRIGHTON, Nicholas
GOODEARL, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 1999-09-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 44; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-09-766-511B-55
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APPLICANT:
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ORGANISM: Homo sapiens
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; ORGANISM: Homo sapiens
US-10-741-790-108
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Best Local Similarity
                 ; OKGANISM: nomo
US-09-759-130B-108
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APPLICANT: Goodearl, Andrew
APPLICANT: Goodearl, Andrew
APPLICANT: Goodearl, Douglas A
TITLE OF INVENTION: NOYEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: NOYEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
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TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
TITLE OF INVENTION: UNMERR: US 09/479,249
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-06-24
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 1999-06-19
PRIOR FILING DATE: 1999-06-10
PRIOR PRILCATION NUMBER: US 09/602,871
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
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PRIOR FILING DATE: 1999-09-10
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                                                                                                                                                                                                                                                                                                                                                                 54 CASRS--ADQIVLCQSEWLKYQGKCYWFSNEMKSWSDSYVYCLERKSHLLIHDQLEMAF 111
                                                                                                                                                                                                                                                                                                                                                                                                                                        122 FOEYVGE-DFYWIGLRDID---GWRWEDGPALSISIL-----SNSVVQKCGTIHRCGL 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                 17;
                                                                                                                                                                                                                              Length 182;
                                                                                                                                                                                                                                                                              59; Indels
                                                                                                                                                                                                                     Query Match
15.9%; Score 164.5; DB 14;
Best Local Similarity 26.9%; Pred. No. 7.7e-09;
Matches 36; Conservative 22; Mismatches 59; 1
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% Sequence 108, Application US/09759130B

% Publication No. US20030022279A1

% EBUREAL INFORMATION:

% APPLICANT: Millennium Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCarthy, Sean A
Fraser, Christopher C
Sharp, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mackay, Charles R
Myers, Paul S
Leiby, Kevin R
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Goodearl, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  171 HASSCEVALOWICE 184
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Kirst, Susan J
NUMBER OF SEQ ID NOS: 646
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 310
LENGTH: 182
                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-125-540-310
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LENGTH: 145
                                                                                                            TYPE: PRT
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
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APPLICANT: Mackay, Charles R
APPLICANT: Myers, Paul S
APPLICANT: Leiby, Kevin R
APPLICANT: Leiby, Kevin R
APPLICANT: Wrighton, Nicolas
APPLICANT: Goodearl, Andrew
APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
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                                                                                                                                                                                                                                                                                                                                                  48 SWNESRDFCKGKGSTLAIVNTPEKLKFLQDITDAEKYFIGLIYHREEKRWRWINNSVFNG 107
                                                                                                                                        40 MVALGLITVIL----MSL-LLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKR 94
                                                                                                                                                                                                                47
                                                                                                                                                                                       -----FCPKDWEFYQARCFFLSTSES
   Length 145;
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                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 NVTNQNFNCATI---GLTKTFDAASCDISYRRICEK 142
                                                                                                                                                                                                                                                                                                                                                                                                                   152 SILSNSVVQKCGTIHRCGL----HASSCEVALQWICEK 185
Query Match
15.7%; Score 163; DB 10;
Best Local Similarity 28.5%; Pred. No. 8.4e-09;
Matches 45; Conservative 25; Mismatches 56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE REFERENCE: MPIO0-5350MIM
CURRENT APPLICATION NUMBER: US/10/741,790
CURRENT PILING DATE: 2003-12-19
PRIOR PRIOR DATE: 2000-10-07
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-04-27
PRIOR FILING DATE: 2000-05-24
PRIOR PILING DATE: 2000-05-24
PRIOR PILING DATE: 2000-05-24
PRIOR PILING DATE: 1999-06-14
PRIOR PILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-29
PRIOR PELING DATE: 1999-06-29
PRIOR PELING DATE: 1999-06-29
PRIOR PELING DATE: 1999-06-29
PRIOR PELING DATE: 1999-06-29
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR PILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR PILING DATE: 1999-09-10
PRIOR PILING DATE: 1999-09-10
PRIOR PILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-09-10
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 2000-06-23
PRIOR FILING DATE: 1999-10-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Millennium Pharmaceuticals, Inc. APPLICANT: McCarthy, Sean A APPLICANT: Fraser, Christopher C APPLICANT: Sharp, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-10-19
NUMBER OF SEQ ID NOS: 460
SOFIWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 108
                                                                                                                                                                                           Sequence 108, Application US/10741790
Publication No. US20040121396A1
GENERAL INFORMATION:
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Kirst, Susan J
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Tue Aug 10 17:15:56 2004

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US-09-759-130B-83
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APPLICANT:
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APPLICANT: Treacy, Maurice
APPLICANT: Treacy, Maurice
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Spaulding, Vikki
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Relleher, Kerry S.
APPLICANT: Relleher, Kerry S.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: G1 6000-L0A
CURRENT APPLICATION NUMBER: U5/10/114,893
CURRENT FILING DATE: 1999-10-06
BARLIER APPLICATION NUMBER: 09/413,232
BARLIER PILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
NUMBER OF SEQ ID NOS: 321
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                                         94
                                                                                ----FCPKDWEFYQARCFFLSTSES 47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         40 MVALGLITVIL----MSL-LLYQRTLCCGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKR
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  Gaps
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  32;
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Llarity 26.2%; Pred. No. 1.8e-08;
Conservative 27; Mismatches 67; Indels 24
  56; Indels
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                                                                                                                                                                                                                                   108 NVTNQNQNFNCATI---GLTKTFDAASCDISYRRICEK 142
                                                                                                                                                                                                           152 SILSNSVVQKCGTIHRCGL----HASSCEVALQWICEK 185
  25; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Chalus, Lionel
APPLICANT: Quan, Ahn B.
APPLICANT: Bates, Blizabeth Ester Mary
APPLICANT: Gorman, Daniel M.
APPLICANT: Saeland, Sem
                                                                                                                                                                                                                                                                                                                                                     ; Sequence 22, Application US/10114893; Publication No. US20020193567A1; GENERAL INFORMATION:
                                                                     Sequence 2, Application US/10270470 Publication No. US20030162955A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Jacobs, Kenneth
APPLICANT: MCOSY, JOHN M.
APPLICANT: LaVallie, Edward R.
APPLICANT: Collins-Racie, Lisa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Ver. 2.0
  45; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: LaVallie, Edw.
APPLICANT: Collins-Racie
APPLICANT: Evans, Cheryl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-114-893-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                            RESULT 10
US-10-114-893-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
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US-10-270-470-2
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APPLICANT: HOLICANT: DOUGLAS A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: BROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
TITLE OF INVENTION: USES.
CURRENT APPLICATION NUMBER: US /09/159,130B
CURRENT APPLICATION NUMBER: US 09/479,249
PRIOR FILING DATE: 2000-01-07
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 1000-05-14
PRIOR APPLICATION NUMBER: US 09/596,194
PRIOR PILING DATE: 1999-06-14
PRIOR PILING DATE: 1999-06-29
PRIOR FILING DATE: 1999-06-30
PRIOR PILING DATE: 1000-07-14
PRIOR PELING DATE: 1000-07-14
PRIOR PELING DATE: 1000-07-14
PRIOR PELING DATE: 1000-06-30
PRIOR FILING DATE: 1000-06-30
PRIOR FILING DATE: 2000-06-30
APPLICANT: Lebecque, Serge J.E.
APPLICANT: Phillips, Joseph H.
TITLE OF INVENTION: ISOLATED MAMMALIAN MEMBRANE PROTEIN GENES; RELATED REAGENTS
FILE REFERENCE: DX0802QF.
CURRENT APPLICATION NUMBER: US/10/270,470
CURRENT FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-16
PRIOR FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 10
SOOTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 162
LENGTH: 162
TYPE: PRI
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APPLICANT: Milennium Pharmaceuticals, Inc.
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Fraser, Christopher C
Sharp, John D
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Myers, Paul S
Leiby, Kevin R
Wrighton, Nicolas
Goodearl, Andrew
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Kirst, Susan J
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Best Local Similarity
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NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version 4.0
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SOFTWARE: PatentIn version 3.2
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                                                                LENGTH: 188
TYPE: PRT
ORGANISM: Homo sapiens
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Matches 47; Conserv
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Matches 36; Conserv
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US-10-335-009-4
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                          SOFTWARE: F
SEQ ID NO 83
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TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPBUTIC, AND OTHER
TITLE OF INVENTION: USES.
                                                                                                                                                                                                                                                                                                                                                                  71 QC--SRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGE 128
                                                                                                                                                                                                                                                                                                                                                                                                        65 RSYGTVCPKDWEFYQARCFFLSTSESSWNESRDFCKGKGSTLAIVNTPEKLKFLQDITDA 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                  129 DFYWIGL----HASSCEVALOW 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               64
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                                                                                                                                                                                                                                          41;
                                                                                                                                                                                           15.4%; Score 159.5; DB 10; Length 188; nlarity 25.5%; Pred. No. 2.6e-08; Conservative 31; Mismatches 65; Indels 41;
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FILE REFERENCE: MPIOO-535CMNIM
CURRENT APPLICATION UNDERE: US/10/741,790
CURRENT APPLICATION UNDERE: US/10/741,790
CURRENT FILING DATE: 2003-12-19
PRIOR APPLICATION NUMBER: US 09/479,249
PRIOR PILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR PILING DATE: 2000-04-27
PRIOR PELING DATE: 2000-04-27
PRIOR PELING DATE: 2000-05-24
PRIOR FILING DATE: 1999-06-14
PRIOR FILING DATE: 1999-06-14
PRIOR APPLICATION NUMBER: US 09/56,194
PRIOR PELING DATE: 1999-06-14
PRIOR PELING DATE: 1999-06-29
PRIOR PELING DATE: 1999-06-29
PRIOR PELING DATE: 1999-06-29
PRIOR PELING DATE: 1999-06-29
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PRIOR PELING DATE: 1999-06-30
PRIOR PELING DATE: 1999-06-30
PRIOR PELING DATE: 1999-06-30
PRIOR PELING DATE: 1999-01-0
                 NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 83
TRNGTH: 188
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 83, Application US/10741790
Publication No. US20040121396A1
GENERAL INFORMATION
APPLICANT: Milennium Pharmaceuticals, Inc
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Kirst, Susan J
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Mackay, Charles R
APPLICANT: Leiby, Kevin R
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Goodearl, Andrew
PRIOR FILING DATE: 1999-10-19
                                                                                                                            ORGANISM: Homo sapiens
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Best Local Similarity
Matches 47; Conserv
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APPLICANT:
APPLICANT:
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APPLICANT:
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                                                                                                                                                                                                                            71 QC--SRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGE 128
                                                                                                                                                                                                                                                                                                                                        129 DFYWIGL----RDIDGWRWEDGPALSLSILSNSVVQKCGTIHRCGL----HASSCEVALQW 181
                                                                                                                                                                                                                                                                                                                                                                        62 CGSKGFMCSQCSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNL 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63 LLRYKGPSDHWIGLSREQGGPWKWINGTEWTRQFPILGAG-----GCAYLNDKGASS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 FQEYVGEDFYWIGLRDIDG--WRWEDG------PALSLSILSNSVVQKCGTIHRCGLHA 172
                                                                                                                                                                        64
                                                                                                                                                    4 CHQEPSVCLQAA-CPESWIGFQRKCFYFSDDTKNWTSSQRFCDSQDADLAQVESFQELNF
                                                             41; Gaps
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APPLICANT: POTUMEJIOOF, STATE SPECIAL S.
TITLE OF INVENTION: LLT USES THEREOF IN IMMUNE SYSTEM MODULATION
FILE REFERENCE: 11707-102/469687-7
CURRENT APPLICATION NUMBER: US/10/335,009
CURRENT PILING DATE: 2002-12-31
PRIOR APPLICATION NUMBER: US 09/475,365
PRIOR FILING DATE: 1999-12-30
        DB 16; Length 188;
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                                                             65; Indels
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                                                                                                                 --YORTLCCGS
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ch 15.4%; Score 159.5; DB : 1. Similarity 25.5%; Pred. No. 2.6e-08, 47; Conservative 31; Mismatches 65
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GENERAL INFORMATION: APPLICANT: Kaser, Matthew R.
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Publication No. US20040001804A1
GENERAL INFORMATION:
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TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES FILE REFERENCE: PA-0035 US
CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT APPLICATION NUMBER: US/09/919,039
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER: OF SEQ ID NOS: 401
SEQ ID NO 130
LENGTHE: 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             81 RNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67 GYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24 WK-VKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFM--CSQCSRCPNLWM 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9 WRLISGTLGIICLS--LMATLGILLKNSFTKLSIEPAFTPGFNIELQKDSDCCSCQEKWV 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 138 IDGWRWEDGPALSLSILSNSV---VQKCGTIHRCG-LHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     125 HTAMLWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 15.0%; Score 155; DB 10; Length 179; Best Local Similarity 27.0%; Pred. No. 7.3e-08; Matches 47; Conservative 28; Mismatches 85; Indels 1-
                                                                                                                                                                                                                                                                                                                                                NAME/KRY: misc feature; OTHER INFORMATION: Incyte ID No. US20030108871A1 516300CD1
US-09-919-039-130
                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Search completed: August 10, 2004, 16:53:37 Job time: 39.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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PCT-US95-04258-5
PCT-US95-04258-6
US-09-722-126A-6
US-09-531-056A-23
US-08-722-4268-8
US-08-772-440-21
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US-08-133-788-3
US-09-113-788-3
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US-09-113-788-3
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US-09-113-788-3
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APPLICANT: PECHT, Israel
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: PUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
STREET: 419 Seventh Street N.W., Ste. 300
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER REALABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: EL PO Compatible
COMPUTER: TEM PC Compatible
OPERATURG SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
CLASSIFICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
FILING DATE: 06-APR-1995
FILING DATE: 08-APR-1995
FILING DATE: 08-APR-1995
FILING DATE: 08-APR-1995
FILING DATE: 08-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER I.
NAME: RECOMPY, ROGER I.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1036; DB 3;
Pred. No. 1.3e-105;
                US-09-531-056A-15
US-09-531-056A-15
US-08-772-440-23
US-08-772-440-23
US-08-772-440-14
US-09-534-22
US-07-614-45A-22
US-08-481-676-2
US-08-481-676-2
US-09-535-521-11
US-09-535-521-11
US-09-535-521-11
US-09-531-056A-21
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Application US/08722126A Patent No. 6034227 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:

APPLICANT: PECHT, Israel

APPLICANT: GUTHMANN, Marcelo D.

APPLICANT: TAL, Michael

TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELI

TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)

NUMBER OF SEQUENCES: 20

CORRESPONDENCES: ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MG-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FT.ING DATE: 08-OCT-1996
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Best Local Similarity 100.0%; Pred. No. 9.7e-64;
Matches 114; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C. STREET: 419 Seventh Street N.W., Ste. 300 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                         Sequence 6, Application US/08722126A Patent No. 6034227
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REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: PE
TELECOMMUNICATION:
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amino acid
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PCT-US95-04258-6
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                                                               1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTL
                                                                                                                        1 MADNSIYSTLELPAAPRVQDDSRWKVKAVLHRPCVSYLVMVALGLITVILMSLLLYORTL
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   Gaps
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WEDIUM TYPE: Floppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Ploppy disk
COMPUTER: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FLING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FLING DATE: 08-APR-1994
ATTORNEY, ROGET L.
NAME: BROWPY, ROGET L.
REGISTRATION NUMBER: 25,618
0; Indels
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FUNCTION-ASSOCIATED ANTIGEN (MAFA)
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419 Seventh Street, N.W., Suite 300
   Mismatches
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GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE
TITLE OF INVENTION: FUNCTION-ASSOC
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
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TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
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INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS: LENGTH: 188 amino acids TYPE: amino acid
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Best Local Similarity 100.
Matches 188; Conservative
Matches 188; Conservative
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181 WICEKVLP 188
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PCT-US95-04258-5
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                                               0; Gaps
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Length 76;
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: PECHT, Israel
APPLICANT: GUTHMANN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: A LONGTION - ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/722,126A
FILING DATE: 08-OCT-1996
CLASSIFICATION: 536
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16.1%; Score 166.5; DB 3;
Best Local Similarity 27.4%; Pred. No. 1.1e-10;
Matches 31; Conservative 22; Mismatches 57;
                                            15;
Query Match 26.4%; Score 273; DB 4;
Best Local Similarity 59.7%; Pred. No. 1.4e-22;
Matches 43; Conservative 14; Mismatches 15
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CLASSIPICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1L 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGRNT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                           Sequence 8, Application US/08722126A Patent No. 6034227 GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: PER
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy
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STRANDEDNESS: si
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APPLICANT: Bristol-Myers Squibb Company
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: DAM MOLECULES ENCODING HUMAN CLAX PROTEINS AND THEIR SOLUBLE FUSI
TITLE OF INVENTION: PROTEINS
FILE REFERENCE: DB20 NP
CURRENT APPLICATION NUMBER: US/09/531,056A
CURRENT FILING DATE: 2000-03-20
NUMBER OF SEQ ID NOS: 24
SOFTWARE: Patentin version 3.0
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Pred. No. 9.7e-64;
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                                                                      A DNA MOLECULE ENCODING A MAST CELL FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMFUTER: IBM PC compatible
COMFATING SYSTEM: PC-DOS/MS-DOS
SOFRAARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                   STREET: 419 Seventh Street, N.W., Suite 300 CITY: Mashington STATE: D.C. STATE: D.C. COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62.8%; Scor.
100.0%; Pred. No. ..
0; Mismatches
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FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23, Application US/09531056A Patent No. 6455683
  Sequence 6, Application PC/TUS9504258
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: A DNA MOLECULI
TITLE OF INVENTION: FUNCTION-ASSO
                                                                                                                 NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: BROWDY, ROGER L. REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 248633
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 114; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-531-056A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                          COUNTRY: US
ZIP: 20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 5
US-09-531-056A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US95-04258-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 23
LENGTH: 76
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Dp Š Q

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50 LMSLLLYQRTLCCGSKGFMCSQ----CSRCPNLWMRNGSHCYYFSMEKRDWNSSLKFCAD 105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |:||:
68 MGAHLVVINTEAEQNFITQQINESLSYFLGLSDPQGNGKWQWIDDTPFSQNVRFWHPHEP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LYELHTYHSSLTCFSEGTMVSEKMWGC--CPNHWKSFGSSCYLLSTKENFWSTSEGNCVQ 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                            COMPUTER READABLE FURM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOUTHMER: Datentin Release #1.0, Version #1.30
SOUTHMENT APELICATION DATA:
APPLICATION NUMBER: US/08/772_440
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PATACK: DATA US.
REGISTRATION NUMBER: 32_165
REFERENCE/DOCKET NUMBER: 32_165
REFERENCE/DOCKET NUMBER: 32_165
REFERENCE/DOCKET NUMBER: 32_165
REFERENCE/DOCKET NUMBER: 32_165
RELEPHONINICATION INFORMATION:
TELLECOMMUNICATION INFORMATION:
TELLEPAK: 512/4/18_300
ITELEPAK: 512/4/18_300
ITELEPAK: S12/4/18_300
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
TENNING OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OF THE OFFICE OFFICE OF THE OFFICE OF THE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFFICE OFF
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Patent No. 5792648
CENEAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Al-Young, Janice
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF EGUURCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 15.3%; Score 158.5; DB 3; Best Local Similarity 28.6%; Pred. No. 1.3e-09; Matches 44; Conservative 23; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    156 NSVVQKCGTI-----HRCGLHASSCEVALQWICE 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: FRACER: DOS
SOFTWARE: FRACERO VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/690,095
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings I....
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0110 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Incyte Pharmace
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 167 amino acids
TYPE: amino acid
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.
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ZIP: 94304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-772-440-21
COUNTRY:
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Patent No. 6046188

GENERAL INFORMATION:
APPLICANT: Ataicumi, Kiyoshi
APPLICANT: Takashima, Akira
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES
TITLE OF INVENTION: TERROF
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75 CPNLWMRNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 27.4%; Pred. No. 1.1e-10;
Matches 31; Conservative 22; Mismatches 57; Indels 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER TEALAGED FORM:
MEDIUM TYPE: ELOppy disk
COMPUTER: IBM PC compatible
ODERATING SYSTEM: PC-DOS/MS-DOS
ODERATING SYSTEM: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/04258
FILING DATE: 06-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 109257
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGET L.
REGISERNICE/DOCKET NUMBER: PECHT=1 PCT
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     A DNA MOLECULE ENCODING A MAST CELL
FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                                                                                                                                         STREET: 419 Seventh Street, N.W., Suite 300 CITY: Washington
                                                                              ; Sequence 8, Application PC/TUS9504258
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: A DNA MOLECULE F
; TITLE OF INVENTION: FUNCTION-ASSOCIA
; NUMBER OF SEQUENCES:
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMBRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 115 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 248633
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Houston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20004
                                                 PCT-US95-04258-8
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14;

Indels

Length 179;

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67 GYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSEE 124
                                                                                                                                                                                                                                                                                                         81 RNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RD 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            24 WK-VKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFM--CSQCSRCPNLWM 80
                                                                                                                                                                                                                      24 WK-VKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFM--CSQCSRCPNLWM 80
                                                                                                                                                                                                                                              125 HTAMLMENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQQL 178
                                                                                                                                                                                                                                                                                                                                                                                            138 IDGWRWEDGPALSLSILSNSV---VOKCGTIHRCG-LHASSCEVALQWICEKVL 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85; Indels
                                                                                                                                                                             85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15.0%; Score 155; DB 2;
ilarity 27.0%; Pred. No. 3.5e-09;
Conservative 28; Mismatches 85;
                                                                                                                                Query Match
Best Local Similarity 27.0%; Pred. No. 3.5e-09;
Matches 47; Conservative 28; Mismatches 85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Goli, Surya K.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
OWRER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE DOCKET NUMBER: PF-0095-1 CIP
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: Incyte Pharmaceuticals, Inc. 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,342
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08688342
Patent No. 5871964
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM Compatible
LENGTH: 179 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     single
                                                               MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COM
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 3174 Por
CITY: Palo Alto
STATE: CA
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Grone: 1098616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                          US-08-650-578-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JS-08-688-342-3
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                                                                                                                                                                                                                                                                                                                                                                                                                 24 WK-VKAVLHRPCVSYLVMVALGLLTVILMSLLLYQRTLCCGSKGFM--CSQCSRCPNLWM 80
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                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Best Local Similarity 27.0%; Pred. No. 3.5e-09;
Matches 47; Conservative 28; Mismatches 85; Indels
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APPLICANT: LopeZ-Botet, Miguel
APPLICANT: Phillips Jr., Joseph H.
APPLICANT: Lanier, Lewis L.
TITLE OF INVENTION: Purified Mammalian NK Antigens and
TITLE OF INVENTION: Related Reagents
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSEE: DNAX Research Institute
F: 901 California Avenue
Palo Alto
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/175,339
FILING DATE: 29-DEC-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/650,578 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08650578
Patent No. 5811284
GENERAL INFORMATION
APPLICANT: Chang, Chiwen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34,090
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
         TELECOMMUNICATION INFORMATION:
                        TELEPANE: 415-855-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                              LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      415-496-1200
                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                 GenBank
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ZIP: 94304-1104
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LIBRARY: General 1098617
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14;

Length 179;

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81 RNGSHCYYFSMEKRDWNSSLKFCADKGSHLLIFPDNQGVNLFQBYVGEDFYWIGL---RD 137
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                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Al-Young, Janice
APPLICANT: Al-Young, Janice
APPLICANT: Goli, Surya K.
TITLE OF INVENTION: NOVEL HUMAN MACROPHAGE ANTIGEN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF-0110 US
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/690,095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 14
US-08-722-126A-9
; Sequence 9, Application US/08722126A
; Batent No. 6034227
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 1.5 CURRENT APPLICATION DATA:
                                                                                                                                      Sequence 9, Application US/09113789
Patent No. 6034219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: PF-(
TELECOMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEPAX: 415-845-4166
INFORMATION FOR END NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IBM Compatible
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TYPE: amino acid
STRANDEDNESS: single
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Matches 47; Conservative
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IMMEDIATE SOURCE:
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                                                                                           RESULT 13
US-09-113-789-9
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                                                                81 RNGSHCYYFSMEKRDWNSSLKFCADKGSHLLTFPDNQGVNLFQEYVGEDFYWIGL---RD 137
                                                                                                      67 GYRCNCYFISSEQKTWNESRHLCASQKSSLLQLQNTDELDFMSS--SQQFYWIGLSYSBE 124
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                                                                                                                                                   138 IDGWRWEDGPALSLSILSNSV---VQKCGTIHRCG-LHASSCEVALQWICEKVL 187
                                                                                                                                                                                     125 HTAWLWENGSALSQYLFPSFETFNTKNCIAYNPNGNALDESCEDKNRYICKQOL 178
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15.0%; Score 155; DB 2; Length 179;
Best Local Similarity 27.0%; Pred. No. 3.5e-09;
Matches 47; Conservative 28; Mismatches 85; Indels
                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Au-Young, Janice
APPLICANT: Cocks, Benjamin G.
APPLICANT: Gocks, Benjamin G.
APPLICANT: Hillman, Jennifer L.
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF-0095-1 CIP
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SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/113,788
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/688,342
                                                                                                                                                                                                                                                                                                       Sequence 3, Application US/09113788
Patent No. 5969104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BILLINGS, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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ZIF: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
"ANDIUM TYPE: Diskette
"ANDIUM TYPE: DOS
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ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    415-845-4166
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: peptide IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LIBRARY: GenBank
CLONE: 1098616
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STATE: C
COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ch 14.8%; Score 153; DB 3; Length 122; Similarity 27.9%; Pred. No. 3.5e-09; 34; Conservative 22; Mismatches 56; Indels
        APPLICANT: GUTHMAIN, Marcelo D.
APPLICANT: TAL, Michael
TITLE OF INVENTION: A DNA MOLECULE ENCODING A MAST CELL
TITLE OF INVENTION: FUNCTION-ASSOCIATED ANTIGEN (MAFA)
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A DNA MOLECULE ENCODING A MAST CELL
FUNCTION-ASSOCIATED ANTIGEN (MAFA)
                                                                                                                                                                                                                                        COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IRM PC compatible

COMFUTER: IRM PC compatible

COMFORTER: IRM PC compatible

COMFORTER: IRM PC compatible

COMFORTER: IRM PC compatible

COMFORTER: IRM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/722,126A

FILING DATE: 06-APR-1995

PRIOR APPLICATION NUMBER: IL 109257

FILING DATE: 06-APR-1994

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, ROGET L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: PECHT=1A

TELECOMMUNICATION NUMBER: 25,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
TITLE OF INVENTION: A DNA MOLECULE ENCODING A
TITLE OF INVENTION: PUNCTION-ASSOCIATED ANTIGH
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
                                                                                                                                            E: BROWDY AND NEIMARK, P.L.L.C.
419 Seventh Street N.W., Ste. 300
                                                                                                                                                                                                                               UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 9, Application PC/TUS9504258 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (202) 628-5197
TELEFAX: (202) 737-3528
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     122 amino acids
PECHT, Israel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                              STREET: 419 Seven
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                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
PCT-US95-04258-9
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local 9
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 10, 2004, 16:11:32; Search time 32.7823 Seconds (without alignments) 1819.059 Million cell updates/sec Run on:

1 MIDSVIYSMLELPTATQAQN......GLQASSCEVPLHGVCKKVRL 189 US-09-811-367B-1 1023 Perfect score:

Gapop 10.0 , Gapext 0.5 BLOSUM62 Scoring table:

Sequence:

Title:

Total number of hits satisfying chosen parameters: 1017041 seqs, 315518202 residues Searched:

1017041

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

SPIREMBL 25:* Database

sp_invertebrate:*
sp_mammal:*
sp_mhc:*
sp_organelle:*
sp_phage:* sp_vertebrate:*
sp_unclassified:* sp_rvirus:*
sp_bacteriap:* sp_archea:*
sp_bacteria:*
sp_fungi:* sp_rodent:* sp_virus:* sp_plant:* sp_fungi:* sp_human:* 10:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

sp_archeap:*

SUMMARIES		Description	O43198 homo sapien	075613 homo sapien	096e93 homo sapien	088713 mus musculu	064335 rattus norv	Ognzez homo sanien	O9nzs1 homo sapien	080288 0811118 0811	09d403 mis misculus	OSmiOS macaca fasc	09wu32 mus musculu	054872 rattus norv	O8sox1 sus scrofa	O9mzk3 macaca mula	012918 homo sanien	Q8mjh7 pongo pygma
		ΔI	043198		Ф96Е93			_	_			_	Q9WU32	054872	Q8SPX1	O9MZK3	012918	Овмлн7
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		Match Length DB	189	189	195	188	188	231	181	200	275	231	227	231	200	231	225	233
•	* Query	Match	100.0	98.4	97.2	53.6	51.4	22.1	22.0	21.7	21.5	21.4	20.5	20.5				
		Score	1023	1001	994	548.5	525.5	226	225	222	219.5	219	210	210	205	201.5	201	201
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Q8mjh6 pongo pygma Q8bhh6 mus musculu Q9gk88 macaca mula	Q9d676 mus musculu Q8vi21 mus musculu O8mii0 popuga pyygma	29mym6 pan troglod 054709 mus musculu	Q9mzk2 macaca mula Q91zw5 mus musculu	Operate macaca musc Operate musculu	Q91zw9 mus musculu	Q8mjh5 pongo pygma O8mjh8 pongo pygma	pongo	P79391 bos taurus	Q91zw7 mus musculu O9wii31 mis misculu		O54871 rattus norv	Q95mq1 bos taurus	OBmill nongo bydma	OBMIIS DODGO DVGMA	pongo	
овмлне оввнне озсквя	Q9D676 Q8VI21 Q8MITO	Q9MYM6 O54709	Q9MZKZ Q91ZW5	Q9Z202	Q91ZW9	Q8MJH5 Q8MJH8	Q8MJH9 090636	P79391	Q91ZW7 O9WU31	Q95L94	054871	Q95MQ1	OBMJII	QBMJI3	Q8MHY8	Овмлно
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ALIGNMENTS

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TISSUE=Lung;

W MEDLINE-98438735; PubMed-9765598;

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Laners M.-Laners L.A.G., Williams D.H.;

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Eukomosta, Metanda...
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 189 AA; 21079 MW; 15E042AD40B2B4F6 CRC64;
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Last annotation update)
                                                                                                                                            189 AA.
                                                                                                                                                                                    043198;
01-0TW-1998 (TrEMBLrel. 06, Created)
01-0TW-1998 (TrEMBLrel. 06, Last seque:
01-0TW-2003 (TrEMBLrel. 24, Last annot:
Mast cell function-associated antigen.
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                                                                                                                                     PRELIMINARY;
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SEQUENCE FROM N.A.
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RESULT 1
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | PEGUENCE FROM N.A. | Editor | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Manager | Mana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
MAPA-L.
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98.4%; Score 1007; DB 4;
Best Local Similarity 98.4%; Pred. No. 4.3e-103;
Matches 186; Conservative 1; Mismatches 2.
                                                                                                                                                                                                                                                                                                                                                               189 AA
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STRAIN-C.B-17 SCID;
MEDLINES-9907194; DubMed=9862378;
Hanke T., Corral L., Vance R.E., Raulet D.H.;
"2F1 antigen, the mouse homolog of the rat '$1', is a lectin-like type II transmembrane receptor expressed by natural killer cells.";
Bur. J. Immunol. 28:4409-4417(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLVITDNQEMS
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01-OCT-2003 (TrEMBLrel. 15, Last annotation update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Mast cell function associated antigen 2F1 (MAFA) (Killer cell lectin-
like receptor G1).
KIRG1 OR MAFA.
Mus musculus (Mouse).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutherla; Rodentia; Sciurognathi; Muridae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
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                                                                                                                                                                                                                                                                                                      Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                               member
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                                                                              01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OECT-2003 (TrEMBLrel. 25, Last annotation update)
Similar to killer cell lectin-like receptor subfamily G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Bone marrow;
Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    195 AA; 21831 MW; 178EE98E08EEC473 CRC64;
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Genew, HGNC:6380; KLRG1.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
InterPro; IPR001364; Lectin C.
Ffam; PR00059, lectin C; 1...
SNART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
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98.4%; Pred. No. 1.2e-101;
live 1; Mismatches 2;
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195 AA
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PRT;
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PRELIMINARY;
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EMEL, X97193; CAA65829.1; JOINED.
EMBL; X97194; CAA65829.1; JOINED.
EMBL; X97195; CAA65829.1; JOINED.
EMBL; X79812; CAA65208.1; -.
PIR; IS9421; IS9421.
GO; GO:0005529; F: sugar binding; IEA.
InterPro; IPR001304; Lectin_C.
Fām; PF00059; lectin_C; I.
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EMBL; AF175206; AAF37804.1; -.
EMBL; AJ305370; CAC29425.1; -.
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MEDLINE-21150889; Pubmed-11265639;
          CAA65829.1; JOINED.
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       EMBL; X97192;
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                                                                                                                                                                STRAIN=129/SvevTACfBr; TISSUE=Spleen,
MEDLINB=21115136; PubMed=11220622;
Voehringer D., Kaufmann M., Pircher H.;
"Genomic structure, alternative splicing, and physical mapping of the killer cell lectin-like receptor G1 gene (KLRG1), the mouse homologue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SECUENCE FROM N.A.

MEDLINE=96016176; PubMed=7568140;
Guthmann M.D., Tal M., Pecht I.;
Guthmann M.D., Tal M., Pecht I.;
a secretion inhibitory signal transduction molecule on mast cells is another C-type lectin.";
Proc. Natl. Acad. Sci. U.S.A. 92:9397-9401(1995).

EMBL; X97191; CAA65829.1; -.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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                                                                 Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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Bocek Jr P., Guthmann M.D., Pecht I.;
Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                188 AA; 21396 MW; 876336802EA134F1 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD; MGI:1355294; Klrg1.
GO; GO:0004872; F:receptor activity; IEA.
GO; GO:0005529; F:sugar binding; IEA.
GO; GO:0007157; P:heterophilic cell adhesion; IEA.
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                                                                                                                                                                                                                                                                                                                                               of MAFA.";
Immunogenetics 52:206-211(2001).
                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AF097357; AAD03718.1;
EMBL; AJ010751; CAA09342.1;
EMBL; AF317727; AAK40082.1;
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01,
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SEQUENCE OF 2-188 FROM N.A.
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nes 104; Conservative
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01-NOV-1996 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              180 QWICKKY 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 HGVCKKV 187
                                                                                                                                      SEQUENCE FROM N.A.
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61 CQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMS 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 LLQVFLSEAFCWIGLRNNSGWRWEDGSPLNFSRISSNSFVQTCGAINKNGLQASSCEVPL 180
                                                                                                                                                                                                                                                                                 09
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GO; GO:0005887; C:integral to plasma membrane; TAS.

GO; GO:0004888; F:transmembrane receptor activity; TAS.

GO; GO:0006960; P:antimicrobial humoral response (sensu Inver. . .; TAS.

GO; GO:0007166; P:cell surface receptor linked signal transdu. . .; TAS.
                                                                                                                                                                                                                                                                                                                          1 MTDSVIYSMLELPTATQAQNDYGPQQKSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWIL
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Bur. J. Immunol. 30:568-576(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20135860; PubMed=10671213;
Roda-Navarro P., Arce I., Renedo M., Montgomery K., Kucherlapati R.,
Fernandez-Ruiz E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vitale M., Falco M., Castriconi R., Parolini S., Zambello R., Semenzato G., Biassoni R., Bottino C., Moretta L., Moretta A.; "Identification of NKp80, a novel triggering molecule expressed by human natural killer Cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                    1;
                                                                                                                  51.4%; Score 525.5; DB 11; Length 188; 53.5%; Pred. No. 7.2e-50; ive 29; Mismatches 57; Indels 1;
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
SEQUENCE 188 AA; 21356 MW; \(\overline{7}\)CC8032D4D020B15 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OUN-2003 (TrEMBLrel. 24, Last annotation update)
Lectin-like receptor F1 (Activating coreceptor NKp80)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    231 AA.
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149 IKGPAKENSCAAIKESKIFSETCSSVFKWICQ 180
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                                                                                               Created)
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                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PR00059; lectin c; l. PRINTS; PR00356; ANTIFREEZEII. SMART; SMO0034; CLECT; l.
                                                                                            01-JUN-2003 (TrEMBLrel. 24, 01-JUN-2003 (TrEMBLrel. 24, 01-OCT-2003 (TrEMBLrel. 25,
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SLCHLHKHWVCSR 186
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                                                                    PRELIMINARY;
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01-JUN-2001 (TrEMBLrel
01-OCT-2003 (TrEMBLrel
4933425B16Rik protein.
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SEQUENCE FROM N.A.
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                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                  C-type lectin.
Y-LEC2.
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                                                                                                                                                                                                                                           130 -FCWIGLRNNS---GWRWEDGSPLNFSRISSNSFVQ-----TCGAINKNGLQASSCEVP 179
                                                                                                                                                                                                                                                          44 GLLTAVLLSVLLYQWILCQGSNYSTCASCPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFC 103
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                                                                                                                                     74
                                                                                                                                                              49 GILTLILISLILLVSÓGVLLKCÓKGSCSNATQYEDTGDLKVNNGTRRNISNKDLCASRSA
                                                                                                                                                                                       ----CPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEA
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Eur. J. Immunol. 30:568-576 (2000).

GO: GO: 0016020; C: membrane; TAS.

GO: GO: 0016020; C: membrane; TAS.

GO: GO: 0030106; F: MHC class I receptor activity; TAS.

InterPro: IPR001394; Lectin. C.

SMART; SM00034; CLECT; I.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                            48;
                                                                                  Length 231;
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                                                                                                           Indels
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                                                        26562 MW; A2F7BE6D4341AFDE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNV-2003 (TrEMBLrel. 24, Last annotation update)
Lectin-like receptor F1, splice variant 1 KLRF1-s1.
KLRF1.
                                                                               22.1%; Score 226; DB 4; I 31.2%; Pred. No. 1.2e-16; Live 27; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22.0%; Score 225; DB 4; 33.6%; Pred. No. 1.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VQ----TCGAINKNGLQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                         181 AA.
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Pfam; PF00059; lectin_c; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                    44 GLLTAVLLSVLLY--QWIL--CQG--
                                                                                                                                                                                                                                                                                                                                                                                      PRT;
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MEDLINE=20135860; PubMed=10671213;
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                                                                             Query Match
Best Local Similarity 31.2%
Matches 58; Conservative
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                                                                                                                                                                                                                                                                                              180 LHGVCK 185
                                                                                                                                                                                                                                                                                                                       225 FKWICQ 230
                                                        231 AA;
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                                            Receptor.
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                                                                                                                                                                                                                                                                                                                                                                                                                       Kalser P.;
"Analysis of part of the chicken Rfp-Y region reveals two novel lectin
"Analysis of part of the chicken Rfp-Y region reveals two novel lectin
genes, the first complete genomic sequence of a class I alpha-chain
gene, a truncated class II beta-chain gene, and a large CR1 repeat.";
Submitted (JAN-2003) to the EMBL/GenBank/DDBJ databases.

EMBL, AJ277927; CAD61336.1;
GO; GO:0005529; F:sugar binding; IEA.

GO; GO:0005157; P:heterophilic cell adhesion; IEA.

InterPro; IPR001353; AntifreezelI.

InterPro; IPR001304; Lectin_C.
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                                                                                                                                          Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23 GPQQKS----SSSKPSCSC-----LVAITLGLLTAVLLSVLLYQWILCQGSNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Rogers S., Shaw I., Ross N., Nair V., Rothwell L., Kaufman J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 AA; 22573 MW; 23AA950D113349B8 CRC64;
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.7%; Score 222; DB 13;
27.5%; Pred. No. 2.7e-16;
ive 31; Mismatches 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50041; C TYPE LECTIN 2; 1.
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74

--GSNYSTCASCPS

40;

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75 ----CPDRMMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  130 -FCWIGLRNNS---GWRWEDGSPLN--FSRISSNSFVQTCGAINKNGLQASSCEVPLHGV 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -----LVAITLGLLTAVLL-SVLLYQWILCQGSNY--STCASCPDRWMKYGNH 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              109 DQTVLCQSEWLKYRGKCYWFSNEMKSWSDSYVYCLERKSHLLIIQDELEMAFIQKNLRQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4 ERVTYA--BLKVAKNSRNQHRKPRGPRSSISVIEQEIIYSDFSFQNPSQEHPWICRNCPC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=99190498; PubMed=10092077;
Lohwasser S., Hande P., Mager D.L., Takei F.;
"Cloning of murine NKG2A, B and C: second family of C-type lectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 227;
                                                                                                                                                                                                                                                                                                  21.4%; Score 219; DB 6; Length 231;
                                                                                                                                                                                                                                                                                                                                                        60; Indels
                                                                                                                                                                                                                                          231 AA; 26710 MW; 403C79CA6883C1E7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    227 AA; 25746 MW; 1651968539C28C86 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 20.5%; Score 210; DB 11; )
1 Similarity 27.1%; Pred. No. 6.7e-15;
62; Conservative 33; Mismatches 78;
                                                                                                                                                                                                                                                                                                                       Pred. No. 6.9e-16;
                                                                                                                                                                                                                                                                                                                                                        27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                227 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 DSVIYSMLELPTATQAQNDY----GPQ----
                                   GO; GO:0004872; F:receptor activity; IEA. GO:0005529; F:sugar binding; IEA. InterPro; IPR001304; Lectin_C. Pfam; PF00059; lectin_C; 1. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IEA
                                                                                                                                                                                                                                                                                                                                                                                                             44 GLLTAVLLSVLLY--QWIL--CQ-----
                                                                                                                                                                            PROSITE; PS50041; C TYPE LECTIN 2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            receptors on murine NK cells.";
Eur. J. Immunol. 29.755-761(1999).
EMBL; AF109784; AAD24970.1; -.
MGD; MGI: 13361; Klrcl.
GO; GO:0004872; F:receptor activity;
GO; GO:0005529; F:sugar binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50041; C_TYPE_LECTIN_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1999 (TrEMBLrel. 12, Created) 01-NOV-1999 (TrEMBLrel. 12, Last seg 01-OCT-2003 (TrEMBLrel. 25, Last ann Natural killer cell receptor NKG2B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001304; Lectin_C.
        EMBL; AJ426430; CAD19994.1;
                                                                                                                                                                                                                                                                                                                             30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00059; lectin c; 1. SMART; SM00034; CLECT; 1.
                                                                                                                                                                                                                                                                                                                       Local Similarity 30,28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
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© 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KLRC1 OR NKG2B
                                                                                                                                                                                                                  Receptor.
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                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184
                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                               Agawa T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Shinagawa A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alakawa T., Hara M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburnar M., Batalov S., Casavant T., Rehl P., Lewis S., Matsuo Y., Nikado I., Pesole G., Quackenbush J., Schrim I.M., Staubli F., Suzuki R., Tomita M., Wagner I., Washio T., Sakri K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., Borfelli D., Bojunga N., Carninci P., de Bonaldo M.F., Butk C., Fletcher C., Fujita M., Gariboldi M., Bronstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Horos P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sava K., Storch K., Schoenbach C., Seya T., Shibara Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming I., Winshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Maria Mayshizaki Y.; Ashibar B., Ringual A., Rasegawa Y., Kawaji H., Kohtsuki S., Daver M., Rasella M., Rodriguez C., Whittaker C., Wilming L., Daver M., Rasella M., Rodriguez D., Maria M., Rodriguez I., Shibar B., Ringual M., Rodriguez I., Shibar Storch K.-F., Shibar Storch K.-F., Shibar Storch M., Wang K., Wang K.H., Weitz C., Whittaker C., Wilming L., Maria M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., Mang M., 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68 TCASCPSCPDRWMKYGNHCYYFSV-EEKDWNSSLEFCLARDSHLLVITDNQEMSLL--QV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                125 FLSEAFCWIGLR-NNSG--WRWEDGS-----PINFSRISSNSFVQTCGAINKNGLQASSC 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ---KCNPCPKTWQWYGNSCYYFSINBEKSWSDSRKDCIDKNATLVKIDSTBERDLLQSQL 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16 TQAQNDYGPQQK--SSSSKPSCSCLVAITL-GLLTAVL----LSVLLYQWILCQGSNYS 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    th 21.5%; Score 219.5; DB 11; Length 275; Similarity 31.6%; Pred. No. 7.5e-16; 60; Conservative 34; Mismatches 73; Indels 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Macaca fascicularis NK cell and receptors.";
Submitted (DRC-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C_TYPE_LECTIN_2; 1.
; -31360 MW; -69792BA25C8B5CC2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P23807; IIXX.
MGD; MGI:1918433; 4933425B16Rik.
GO; GO:0005529; F:sugar binding; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                             MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AK016908; BAB30491.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001304; Lectin C.
Pfam; PR00055; lectin C; 1.
SMART; SM00034; CLECT; 1.
PROSITE; PS50041; C_TYPE_LECTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QBMIU5;
01-OCT-2002 (TrEMBLrel. 22,
01-OCT-2002 (TrEMBLrel. 22,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EVPLHGVCKK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cercopithecinae; Macaca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   255 RAEIPWICEK 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=NK lymphocytes;
Biassoni R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 60; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NKp80 NK receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9541;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 10
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66 YSTCAS --- CPSCPDRWMKYGNHCYYFSVEEKDWNSSLEFCLARDSHLLVITDNQE-MSL 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         133 LKOHVGRAEHWIGLKNEDGOTWKWSNGKEFNNWFKLTGS----KNCPFLNSTEVGSMECE 188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13 PTATQAQNDYGP----QQKSSSSKP-SCSC--LVAITLGLLTAVLLSVLLYQWILCQGSN 65
                                                                                                                                                                                                         Yim D., Sotiriadis J., Kim K.-S., Shin S.-C., Jie H.-B., Rothschild M.F., Kim Y.B., "Molecular cloning, expression pattern, and chromosomal mapping of pig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16 PNRGQPSNATGPHFATHHEGSLQVPIPCAVVNVVFITVLITALIALSVGQYN---CPGQY
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Mammalia, Eutheria, Primates, Catarrhini, Cercopithecidae,
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MEDLINE=20322487; PubMed=10866118;
MEDLINE=20322487; PubMed=10866118;
Letvin N.L.; Letvin N.L.;
"Characterization of rhesus monkey CD94/NKG2 family members and identification of novel transmembrane-deleted forms of NKG2-A, B,
Euteleostomi;
Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20.0%; Score 205; DB 6; Length 20.
29.6%; Pred. No. 2.1e-14;
live 27; Mismatches 84; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, AF444233, AAL91546.1; -..
EMBL, AF444233, AAL91546.1; -..
EGO, GO:0005529; Fs:ugar binding; IEA.
InterPro; IRRO01304; Lectin_C.
Pfam; PF00059; lectin_c; 1.
PROSITE; PS00013; CLECT; 1.
PROSITE; PS00013; CTPE LECT; 1.
SEQUENCE 200 AA; 22257 MW; G55E876FE163A57C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenetics 51:496-499 (2000).

EMBL; AF19037; AAF74533.1; -.

HSSP; P22897; IRGG.

GO: GO:0005229; F:sugar binding; IEA.

InterPro; IPR001304; Lectin.C.

Ffam; PF00055; lectin.c; 1...

SMART; SM0034; CLECT; 1.

PROSITE; PSS0041; C.TYPE LECTIN.2; 1.

SRQUENCE 231 AA; 26107 MW; COD307ABE0262DBD CRC64;
                Chordata; Craniata; Vertebrata;
Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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19.7%; Score 201.5; DB 6;
Best Local Similarity 29.8%; Pred. No. 6e-14;
Matches 59; Conservative 30; Mismatches 92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 178 VPLHGVCKK 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
            Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=9823;
                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                         CYYFSVEEKDWNSSLEFCLARDSHLLVITDNQEMSLLQVFLSEAFCWIG-LRNNSG--WR 142
                                                                                                                                                       KGFPSPPEKLIAGTLGLICFVLIVAVVVITTVATPYINYTLSSAQPCPHCPKEWISYSHN 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Berg S.F., Dissen E., Westgaard I.H., Fossum S.;
"Molecular characterization of two genes in the rat homologous to human NKG2.";
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                                                                                                                                                                                                                                                                    143 WEDGSPLNFSRISSNSFVQ-----TCGAINKNGLQASSCEVPLHGVCK 185
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                                                                                                                                                                                                                                                                                                              81; Indels
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Type II membrane protein CD69.
Sus scrofa (Pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-1998 (TrEMBLrel. 06, Last sequence update) 01-OCT-2003 (TrEMBLrel. 25, Last annotation update) Natural killer cell protein group 2-A (Fragment).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eur. J. Immunol. 28:444-450(1998).
EMEL; AF021356; AA440050.1; ---
GO; GO:000529; F:sugar binding; IEA.
InterPro; IPR00235; AntifreeZeII.
InterPro; IPR0039; Lectin.C.
PEAN; PR0059; lectin.C.
PRINTS; PR00556; ANTIFREEZEII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus norvegicus (Rat).
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Matches 54; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       054872;
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=F344;
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111 LVITDNQEMSLLQVFLSEAFCWIGL-RNNSGWRWEDGSPLNFSRLSSNS--FVQTCGAIN 167
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TDSVIYSMLELPTATQAQNDYGPQQ--KSSSSKPSCSCLVAITLGLLTAVLLSVLLYQWI 59
                                            54 VVTGLSVSVT----SLIQKSSIEKCSVDIQQSRNKTTERPGLLNCPIYWQQLREKCLLFS
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K REDLINE=94358407, PubMed=8077657;

K REDLINE=94358407, PubMed=8077657;

Lanier L.L., Chang C., Phillips J.H.;

Lanier L.L., Chang C., Phillips J.H.;

R BEDLINE=13532417-2428 [1949].

L J. Immunol. 15312417-2428 [1994].

R PIR, 138700, 138700.

R PIR, 138700, 138700.

R R GO: GO: 0005530; F:lectin, TAS.

G GO: GO: 0005530; F:lectin, TAS.

GO: GO: 0005530; F:lectin, TAS.

GO: GO: 000166; P:cell surface receptor activity; TAS.

R GO: GO: 000166; P:cell surface receptor linked signal transdu. .; TR

R GO: GO: 000166; P:cell surface receptor linked signal transdu. .; TR

R MRRT; SM00034; CLECT; I.

R PROSITE; PS50041; C_TYPE LECTIN 2; I.
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               000044; CLECL; L. PS50041; C TYPE LECTIN 2; 1. 225 AA; 25415 MW; 01BFA925445B83B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                     168 KNGLQASSCEVPLHGVCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                              211 ARGLKSNQCESTVIYHCK 228
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01-NOV-1996 (TrEMBLrel.
01-JUN-2003 (TrEMBLrel.
HNKR-Pla protein.
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